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OM protein - protein search, using sw model

Run on: December 1, 2004, 11:44:25 ; Search time 468 Seconds
(without alignments)
59.188 Million cell updates/sec

Title: US-10-673-860-3
Perfect score: 113
Sequence: 1 MKRMSLAALTVAGMLAPVATA 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA, Main: *

- 1: /cgn2_6/ptodata/1/paa/pctus COMB.pcp.*
- 2: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
- 3: /cgn2_6/ptodata/1/paa/US07 COMB.pcp.*
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- 35: /cgn2_6/ptodata/1/paa/US39 COMB.pcp.*
- 36: /cgn2_6/ptodata/1/paa/US40 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113	100.0	25	27	US-10-112-488-2
2	113	100.0	25	32	US-10-673-860-3
3	57	50.4	395	21	US-09-738-626-6644
4	57	50.4	395	34	US-10-805-394-6644
5	56	49.6	135	26	US-10-015-127-11497
6	55	48.7	517	30	US-10-449-902-42629
7	55	48.7	526	30	US-10-437-963-190930
8	52	46.0	141	22	US-09-791-537-76056
9	51.5	45.6	87	27	US-10-158-761-12894
10	51	45.1	104	21	US-09-738-626-4865
11	51	45.1	104	34	US-10-805-394-4865
12	51	45.1	107	1	PCT-US99-03265-84
13	51	45.1	107	1	PCT-US99-03268-83
14	51	45.1	107	10	US-08-658-800-84
15	51	45.1	107	10	US-08-659-683-83
16	51	45.1	107	10	US-08-680-573-84
17	51	45.1	107	11	US-08-680-574-83
18	51	45.1	107	11	US-08-729-622-84
19	51	45.1	107	11	US-08-730-510-83
20	51	45.1	107	13	US-08-942-341-84
21	51	45.1	107	13	US-08-942-578-83
22	51	45.1	107	14	US-09-024-753-84
23	51	45.1	107	14	US-09-025-197-83
24	51	45.1	107	21	US-09-724-685-83
25	51	45.1	107	26	US-10-084-843-83
26	51	45.1	107	27	US-10-193-002-84
27	51	45.1	168	1	PCT-US99-03265-95
28	51	45.1	168	1	PCT-US99-03268-100
29	51	45.1	168	10	US-08-658-800-94
30	51	45.1	168	10	US-08-659-683-100
31	51	45.1	168	10	US-08-680-573-94
32	51	45.1	168	10	US-08-680-574-100
33	51	45.1	168	11	US-08-729-622-94
34	51	45.1	168	11	US-08-730-510-100
35	51	45.1	168	13	US-08-942-341-95
36	51	45.1	168	13	US-08-942-578-100
37	51	45.1	168	14	US-09-024-753-95
38	51	45.1	168	14	US-09-025-197-100
39	51	45.1	168	21	US-09-724-685-100
40	51	45.1	168	26	US-10-009-384-19
41	51	45.1	168	26	US-10-080-170-534
42	51	45.1	168	26	US-10-084-843-100
43	51	45.1	168	27	US-10-193-002-95
44	51	45.1	168	30	US-10-468-358-534
45	51	45.1	187	1	PCT-US99-03265-64

ALIGNMENTS

RESULT 1
US-10-112-488-2
; Sequence 2, Application US/10112488
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, Yoshiaki
; APPLICANT: DATE, Masayo
; APPLICANT: UMEZAWA, Yukiko
; APPLICANT: YOKOYAMA, Keiichi
; APPLICANT: MATSUI, Hiroshi
; TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSLUTAMINASE
; FILE REFERENCE: 219286USOCNT
; CURRENT APPLICATION NUMBER: US/10/112,488
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: PCT/JF00/06780
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: JP2000-280098
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: JP11-280098
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 70

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Corynebacterium ammoniagenes
US-10-112-488-2

Query Match      100.0%; Score 113; DB 27; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAAPVATA 25
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Db 1 MKRMKSLAAALTAVAGAMLAAPVATA 25

RESULT 2
US-10-673-860-3
; Sequence 3, Application US/10673860
; GENERAL INFORMATION:
; APPLICANT: Ajinomoto Co., Inc.
; TITLE OF INVENTION: A method of secreting and producing proteins
; FILE REFERENCE: YLJ0182
; CURRENT APPLICATION NUMBER: US/10/673,860
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: JP 2001-98808
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Corynebacterium ammoniagenes
US-10-673-860-3

Query Match      100.0%; Score 113; DB 32; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAAPVATA 25
   |||||
Db 1 MKRMKSLAAALTAVAGAMLAAPVATA 25

RESULT 3
US-09-738-626-6644
; Sequence 6644, Application US/09738626
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6644
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-805-394-6644

Query Match      50.4%; Score 57; DB 34; Length 395;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 KRMKSLAAALTAVAGAMLA 19
   |||||
Db 13 KRLKPLAAAVAVAGVLLA 30

RESULT 4
US-10-805-394-6644
; Sequence 6644, Application US/10805394
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/10/805,394
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6644
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-805-394-6644

Query Match      50.4%; Score 57; DB 34; Length 395;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 KRMKSLAAALTAVAGAMLA 19
   |||||
Db 13 KRLKPLAAAVAVAGVLLA 30

RESULT 5
US-10-015-127-11497
; Sequence 11497, Application US/10015127
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof
; FILE REFERENCE: 38-10(15806)B
; CURRENT APPLICATION NUMBER: US/10/015,127
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/252,455
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 14357
; SEQ ID NO 11497
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Sphingomonas elodea
US-10-015-127-11497
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Query Match 49.6%; Score 56; DB 26; Length 135;
Best Local Similarity 54.5%; Pred. No. 5.5; Mismatches 3; Indels 7; Gaps 0;

Qy 4 MKSLAALTVAGAMLAAPVATA 25
Db 1 MKTILATLLAGALLAAPVANA 22

RESULT 6
US-10-449-902-42629
; Sequence 42629, Application US/10449902
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205V1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42629
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-42629

Query Match 48.7%; Score 55; DB 30; Length 517;
Best Local Similarity 54.2%; Pred. No. 36; Mismatches 4; Indels 7; Gaps 0;

Qy 2 KRMKSLAALTVAGAMLAAPVATA 25
Db 6 RRRRSRAAAVLVAALLLAASAATA 29

RESULT 7
US-10-437-963-190930
; Sequence 190930, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 190930
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(526)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_87298C.1.pep
US-10-437-963-190930

Query Match 48.7%; Score 55; DB 30; Length 526;

Best Local Similarity 54.2%; Pred. No. 37; Mismatches 13; Conservative 7; Indels 0; Gaps 0;

Qy 2 KRMKSLAALTVAGAMLAAPVATA 25
Db 6 RRRRSRAAAVLVAALLLAASAATA 29

RESULT 8
US-09-791-537-76056
; Sequence 76056, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 76056
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Streptomyces aureofaciens
US-09-791-537-76056

Query Match 46.0%; Score 52; DB 22; Length 141;
Best Local Similarity 47.8%; Pred. No. 24; Mismatches 11; Conservative 4; Indels 8; Gaps 0;

Qy 3 RKMKSLAALTVAGAMLAAPVATA 25
Db 6 RLVALAGAAVAATLIAGPVAATA 28

RESULT 9
US-10-156-761-12894
; Sequence 12894, Application US/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12894
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12894

Query Match 45.6%; Score 51.5; DB 27; Length 87;
Best Local Similarity 65.2%; Pred. No. 16; Mismatches 15; Conservative 1; Indels 6; Gaps 1;

Qy 4 MKSLAALTVAGAM-LAAPVATA 25
Db 1 MKSLKAAAVVAGSMVLGAVAPA 23

RESULT 10

US-09-738-626-4865
; Sequence 4865, Application US/09738626
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4865
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4865

Query Match 45.1%; Score 51; DB 21; Length 104;
Best Local Similarity 48.0%; Pred. No. 24;
Matches 1; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGMLAAPVATA 25
DB 2 IKKYLSTIAAVTIASAVLFAFSAQA 26

RESULT 11
US-10-805-394-4865
; Sequence 4865, Application US/10805394
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/10/805,394
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4865
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-805-394-4865

Query Match 45.1%; Score 51; DB 34; Length 104;

Best Local Similarity 48.0%; Pred. No. 24;
Matches 12; Conservative 8; Indels 0; Gaps 0;
QY 1 MKRMKSLAAALTAVAGMLAAPVATA 25
DB 2 IKKYLSTIAAVTIASAVLFAFSAQA 26

RESULT 12
PCT-US99-03265-84
; Sequence 84, Application PC/TUS9903265
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/03265
; FILING DATE: 17-FEB-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/024,753
; FILING DATE: 18-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Laura A. Coruzzi
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 9532-0023-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US99-03265-84

Query Match 45.1%; Score 51; DB 1; Length 107;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGMLAA 20
DB 10 MKMKVKSIAAGLTAAAGAA 29

RESULT 13
PCT-US99-03268-83
; Sequence 83, Application PC/TUS9903268
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/03268
FILING DATE: 17-FEB-1999
CLASSIFICATION: 406
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/025,197
FILING DATE: 18-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9532-0013-228
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US99-03268-83

Query Match 45.1%; Score 51; DB 1; Length 107;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTVAGAMLAA 20
||:|||||:|
Db 10 MKMWKSIAGLTAAAAIGAA 29

RESULT 14
US-08-658-800-84
; Sequence 84, Application US/08658800
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TUBERCULOSIS
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,800
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-658-800-84

Query Match 45.1%; Score 51; DB 10; Length 107;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTVAGAMLAA 20
||:|||||:|
Db 10 MKMWKSIAGLTAAAAIGAA 29

RESULT 15
US-08-659-683-83
; Sequence 83, Application US/08659683
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,683
; FILING DATE: 05-JUN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-659-683-83

Query Match 45.1%; Score 51; DB 10; Length 107;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTVAGAMLAA 20
||:|||||:|
Db 10 MKMWKSIAGLTAAAAIGAA 29

RESULT 16
US-08-680-573-84
; Sequence 84, Application US/08680573
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonia

```

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,573
; FILING DATE: 12-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-680-573-84

Query Match 45.1%; Score 51; DB 10; Length 107;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
Db 10 MKRMKSLAAALTAVAGAMLAA 29

RESULT 17
US-08-680-574-83
; Sequence 83, Application US/08680574
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 133
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,574
; FILING DATE: 12-JUL-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-729-622-84

Query Match 45.1%; Score 51; DB 11; Length 107;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
Db 10 MKRMKSLAAALTAVAGAMLAA 29

RESULT 18
US-08-729-622-84
; Sequence 84, Application US/08729622
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Twardzik, David R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,622
; FILING DATE: 11-OCT-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-729-622-84

Query Match 45.1%; Score 51; DB 11; Length 107;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
Db 10 MKRMKSLAAALTAVAGAMLAA 29
```

RESULT 19
US-08-730-510-83
; Sequence 83, Application US/08730510
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/730,510
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-6031
; TELEFAX: (206) 622-4900
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-730-510-83
Query Match 45.1%; Score 51; DB 11; Length 107;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 MKRMKSLAALTVAGAMLAA 20
Db 10 MKMKVKSIAAGLTAAGAA 29
RESULT 20
US-08-942-341-84
; Sequence 84, Application US/08942341
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle

STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,341
FILING DATE: 01-OCT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-6031
TELEFAX: (206) 622-4900
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-942-341-84
Query Match 45.1%; Score 51; DB 13; Length 107;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 MKRMKSLAALTVAGAMLAA 20
Db 10 MKMKVKSIAAGLTAAGAA 29
RESULT 21
US-08-942-578-83
; Sequence 83, Application US/08942578
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/942,578
; FILING DATE: 01-OCT-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-942-578-83

Query Match 45.1%; Score 51; DB 13; Length 107;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTAVAGAMLAA 20
||:|||||:|:|
Db 10 MKMKVKSIAAGLTAAAGAA 29

RESULT 22

US-09-024-753-84
; Sequence 84, Application US/09024753
; GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 236
CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,753
FILING DATE: 18-FEB-1998
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-024-753-84

Query Match 45.1%; Score 51; DB 14; Length 107;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTAVAGAMLAA 20
||:|||||:|:|
Db 10 MKMKVKSIAAGLTAAAGAA 29

RESULT 23

US-09-025-197-83
; Sequence 83, Application US/09025197
; GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,197
FILING DATE: 18-FEB-1998
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-025-197-83

Query Match 45.1%; Score 51; DB 14; Length 107;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTAVAGAMLAA 20
||:|||||:|:|
Db 10 MKMKVKSIAAGLTAAAGAA 29

RESULT 24

US-09-724-685-83
; Sequence 83, Application US/09724685
; GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir
APPLICANT: Dillon, Davin C.

ADDRESSEE: Campos-Neto, Antonio
TITLE OF INVENTION: Compounds and Methods for
Immunotherapy and Diagnosis of Tuberculosis

NUMBER OF SEQUENCES: 155
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,685
FILING DATE: 28-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/523,436
FILING DATE: 01-SEP-1995
APPLICATION NUMBER: US 08/533,634
FILING DATE: 22-SEP-1995
APPLICATION NUMBER: US 08/620,874
FILING DATE: 22-MAR-1996
APPLICATION NUMBER: US 08/659,683
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: US 08/680,574
FILING DATE: 12-JUL-1996
APPLICATION NUMBER: WO PCT/US96/14674
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: US 08/730,511
FILING DATE: 11-OCT-1996
APPLICATION NUMBER: US 08/818,112
FILING DATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 014058-008561US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-09-724-685-83
Query Match 45.1%; Score 51; DB 21; Length 107;
Best Local Similarity 60.0%; Pred. NO. 24;
Matches 12; Conservative 3; Mismatches 5; Indels 0;
QY 1 MKRWKSLAALTACAMLAA 20
DBD 10 MKRWKSLAAGLTAAAAGAA 29
RESULT 25
US-10-084-843-83
; Sequence 83, Application US/10084843
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Iwardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092


```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/658,800
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-658-800-94

Query Match 45.1%; Score 51; DB 10; Length 168;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
   ||:|||||:|||||:
Db 1 MKMWKSIAGLTAAAGAA 20

RESULT 30
US-08-659-693-100
; Sequence 100, Application US/08659683
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05-JUN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-659-683-100

Query Match 45.1%; Score 51; DB 10; Length 168;

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Best Local Similarity 60.0%; Pred. No. 41;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
   ||:|||||:|||||:
Db 1 MKMWKSIAGLTAAAGAA 20

RESULT 31
US-08-680-573-94
; Sequence 94, Application US/08680573
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, David C.
; APPLICANT: Campos-Neto, Antonio
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,573
; FILING DATE: 12-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-680-573-94

Query Match 45.1%; Score 51; DB 10; Length 168;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
   ||:|||||:|||||:
Db 1 MKMWKSIAGLTAAAGAA 20

RESULT 32
US-08-680-574-100
; Sequence 100, Application US/08680574
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, David C.
; APPLICANT: Campos-Neto, Antonio
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 133
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle

```

STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/680,574
APPLICATION NUMBER: US/08/680,574
FILING DATE: 12-JUL-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-680-574-100

Query Match 45.1%; Score 51; DB 10; Length 168;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTAVAGAMLA 20
Db 1 MKMVKSIAAGLTAAGAAIGAA 20

RESULT 33
US-08-729-622-94
Sequence 94, Application US/08729622
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, David R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,622
FILING DATE: 11-OCT-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-729-622-94

Query Match 45.1%; Score 51; DB 11; Length 168;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTAVAGAMLA 20
Db 1 MKMVKSIAAGLTAAGAAIGAA 20

RESULT 34
US-08-730-510-100
Sequence 100, Application US/08730510
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedwick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/730,510
FILING DATE: 27-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-730-510-100

Query Match 45.1%; Score 51; DB 11; Length 168;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTAVAGAMLA 20
Db 1 MKMVKSIAAGLTAAGAAIGAA 20

RESULT 35
US-08-942-341-95

LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-024-753-95

Query Match 45.1%; Score 51; DB 14; Length 168;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRWKSLAAALTVAGAMLAA 20
||:|||||:
Db 1 MKRWKSLAAAGLTAAGAA 20

RESULT 38

US-09-025-197-100
; Sequence 100, Application US/09025197
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Twardzik, Thomas S.
; APPLICANT: Lodes, Michael J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; City: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 18-FEB-1998

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C8
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-025-197-100

Query Match 45.1%; Score 51; DB 14; Length 168;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRWKSLAAALTVAGAMLAA 20
||:|||||:
Db 1 MKRWKSLAAAGLTAAGAA 20

RESULT 39

US-09-724-685-100
; Sequence 100, Application US/09724685

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir
Dillon, Davin C.
Campos-Neto, Antonio

TITLE OF INVENTION: Compounds and Methods for
Immunotherapy and Diagnosis of Tuberculosis

NUMBER OF SEQUENCES: 155
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,685
FILING DATE: 28-Nov-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/523,436
FILING DATE: 01-SEP-1995
APPLICATION NUMBER: US 08/533,634
FILING DATE: 22-SEP-1995
APPLICATION NUMBER: US 08/520,874
FILING DATE: 22-MAR-1996
APPLICATION NUMBER: US 08/659,683
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: US 08/680,574
FILING DATE: 12-JUL-1996
APPLICATION NUMBER: WO PCT/US96/14674
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: US 08/730,511
FILING DATE: 11-OCT-1996
APPLICATION NUMBER: US 08/818,112
FILING DATE: 13-MAR-1997

ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 014058-008561US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-724-685-100

Query Match 45.1%; Score 51; DB 21; Length 168;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRWKSLAAALTVAGAMLAA 20
||:|||||:
Db 1 MKRWKSLAAAGLTAAGAA 20

RESULT 40
US-10-009-384-19
; Sequence 19, Application US/10009384
; GENERAL INFORMATION:
; APPLICANT: Gennaro, Maria Laura
; APPLICANT: Gomez, Manuel J.
; TITLE OF INVENTION: SECRETED PROTEINS OF MYCOBACTERIUM

; TITLE OF INVENTION: TUBERCULOSIS AND THEIR USE AS VACCINES AND DIAGNOSTIC

; TITLE OF INVENTION: REAGENTS

; FILE REFERENCE: 07763-042001

; CURRENT APPLICATION NUMBER: US/10/009,384

; CURRENT FILING DATE: 2003-10-14

; PRIOR APPLICATION NUMBER: US 60/132,503

; PRIOR FILING DATE: 1999-05-04

; PRIOR APPLICATION NUMBER: US 60/132,479

; PRIOR FILING DATE: 1999-05-04

; NUMBER OF SEQ ID NOS: 94

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 19

; LENGTH: 168

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis

US-10-009-384-19

Query Match 45.1%; Score 51; DB 26; Length 168;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTIVAGAMLAA 20

DB 1 MKQVKSIAAGLTAAAAIGAA 20

Search completed: December 1, 2004, 11:59:31
Job time : 469 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2004, 11:33:34 ; Search time 189 Seconds
(without alignments)
76.108 Million cell updates/sec

Title: US-10-673-860-3
Perfect score: 113
Sequence: 1 MKRMKSLAAALTAVAGMLAAPVATA 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	100.0	358	Q93R90	Q93R90 corynebacte
2	57	50.4	385	Q6M204	Q6M204 corynebacte
3	57	50.4	385	CAF20877	CAF20877 corynebacte
4	57	50.4	395	Q8NLT5	Q8NLT5 corynebacte
5	57	50.4	430	Q84OC2	Q84OC2 cellvibro
6	56	49.6	346	Q7NXL7	Q7NXL7 chromobacte
7	54	47.8	438	Q6SH08	Q6SH08 uncultured
8	54	47.8	438	AAR37811	AAR37811 unculture
9	53	46.9	122	Q715L8	Q715L8 mycobacteri
10	53	46.9	122	AAQ12134	AAQ12134 mycobacte
11	53	46.9	133	Q9YG03	Q9YG03 aeropyrum p
12	53	46.9	333	Q89FK9	Q89FK9 bradyrhizob
13	53	46.9	507	Q50506	Q50506 streptomyc
14	52	46.0	141	RNS3 STRAU	RNS3 STRAU
15	52	46.0	399	Q985D9	Q985D9 streptomyc
16	51.5	45.6	87	Q93HK7	Q93HK7 streptomyc
17	51.5	45.6	948	Q8KQL9	Q8KQL9 saccharopol
18	51	45.1	104	Q8NR31	Q8NR31 corynebacte
19	51	45.1	104	CAF19936	CAF19936 corynebacte
20	51	45.1	168	MB12 MYCTU	MB12 MYCTU
21	51	45.1	248	Q8XVA4	Q8XVA4 ralstonia s
22	51	45.1	431	Q9S3L6	Q9S3L6 bacillus sp
23	51	45.1	434	Q54327	Q54327 bacillus sp
24	51	45.1	482	Q8XTE9	Q8XTE9 ralstonia s
25	50.5	44.7	328	Q7W382	Q7W382 bordetella
26	50.5	44.7	328	Q7W382	Q7W382 bordetella
27	50	44.2	81	Q829D3	Q829D3 streptomyc
28	50	44.2	100	Q9KVG9	Q9KVG9 streptomyc
29	50	44.2	125	RL7 RICPR	RL7 RICPR
30	50	44.2	279	Q8NTB4	Q8NTB4 corynebacte
31	50	44.2	279	CAF19108	CAF19108 corynebacte

32	50	44.2	284	2	Q92MJ0	Q92MJ0 rhizobium m
33	50	44.2	353	2	Q6WIL8	Q6WIL8 rhizobium s
34	50	44.2	353	2	AAQ87350	AAQ87350 rhizobium s
35	50	44.2	431	2	Q91OG9	Q91OG9 streptomyc
36	50	44.2	517	2	Q8XTF1	Q8XTF1 ralstonia s
37	49.5	43.8	185	2	Q73W90	Q73W90 mycobacteri
38	49.5	43.8	185	2	AA505087	AA505087 mycobacte
39	49	43.4	82	2	Q9X9Z2	Q9X9Z2 streptomyc
40	49	43.4	231	2	Q6NIM5	Q6NIM5 rhodospseud
41	49	43.4	231	2	CAE29821	CAE29821 rhodospseu
42	49	43.4	313	1	YDCU ECOLI	YDCU ECOLI
43	49	43.4	313	2	Q7AB55	Q7AB55 escherichia
44	49	43.4	313	2	Q8FHK9	Q8FHK9 escherichia
45	49	43.4	313	2	Q8X9W3	Q8X9W3 escherichia

ALIGNMENTS

RESULT 1

Q93R90

AC Q93R90

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Cell surface protein A.

GN Name=csaA;

OS Corynebacterium ammoniagenes (Brevibacterium ammoniagenes).

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.

OX NCBI_TaxID=1697;

EN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 5872;

RA Usuda Y., Kawasaki H., Utagawa T.;

RT "Characterization of the cell surface protein gene of Corynebacterium ammoniagenes.";

RL Biochim. Biophys. Acta 1552:138-141 (2001).

DR EMBL; AB055224; BAB62413.1; -.

DR InterPro; IPR000801; Esterase_put.

DR Pfam; PF00756; Esterase; 1.

RT CHAIN 26 358

SQ SEQUENCE 358 AA; 39081 MW; 0785CA660295A1C-GR64;

Query Match Similarity 100.0%; Score 113; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKRMKSLAAALTAVAGMLAAPVATA 25
Db	1	MKRMKSLAAALTAVAGMLAAPVATA 25

RESULT 2

Q6M204

AC Q6M204

DT 05-JUL-2004 (Tremblrel. 27, Created)

DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)

DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

DE BETA-N-ACETYLGLUCOSAMINIDASE (EC 3.2.1.52).

GN Name=nagA2; OrderedLocusNames=c93158;

OS Corynebacterium glutamicum (Brevibacterium flavum).

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.

OX NCBI_TaxID=1718;

EN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;

RA Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M., Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,

Query Match Similarity 100.0%; Score 385 AA.

RA Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
RA McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Puhler A.,
RA Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I.,
RA Tauch A.,
RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence
RT and its impact on the production of L-aspartate-derived amino acids
RT and vitamins.",
RL J. Biotechnol. 104:5-25(2003).
DR EMBL: BX927156; CAF20877.1; -
DR GO: GO:0004563; F:beta-N-acetylhexosaminidase activity; IEA.
DR GO: GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR001764; Glyco_hydro_3N.
DR Pfam: PF00933; Glyco_hydro_3; 1.
DR Glycosidase; Hydrolase.
SQ SEQUENCE 385 AA; 40473 MW; 367F80C810D53849 CRC64;
Query Match 50.4%; Score 57; DB 2; Length 385;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 KRMSLAALAAALTVAGAMLA 19
|||:||||:||||:|
Db 3 KRLKPLAAAVAGVLLA 20
|||:||||:||||:|
RESULT 3
CAF20877 PRELIMINARY; PRT; 385 AA.
AC CAF20877;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE BETA-N-ACETYLGLUCOSAMINIDASE (EC 3.2.1.52).
GN NAGA2 OR CG3158.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX PubMed=12948626;
RA Kalincowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
RA Burkowski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
RA Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
RA McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Puhler A.,
RA Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I.,
RA Tauch A.,
RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence
RT and its impact on the production of L-aspartate-derived amino acids
RT and vitamins.",
RL J. Biotechnol. 104:5-25(2003).
DR EMBL: BX927156; CAF20877.1; -
DR Glycosidase; Hydrolase.
SQ SEQUENCE 385 AA; 40473 MW; 367F80C810D53849 CRC64;
Query Match 50.4%; Score 57; DB 2; Length 385;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 KRMSLAALAAALTVAGAMLA 19
|||:||||:||||:|
Db 3 KRLKPLAAAVAGVLLA 20
|||:||||:||||:|
RESULT 4
Q8NLT5 PRELIMINARY; PRT; 395 AA.
AC Q8NLT5;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Beta-glucosidase-related glycosidases (EC 3.2.1.30).
GN OrderedLocusNames=Cgl12852;
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP005283; BAC00246.1; -
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl bonds; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR001764; Glyco_hydro_3N.
DR Pfam: PF00933; Glyco_hydro_3; 1.
DR Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 395 AA; 41554 MW; FBF35F878C4F06AD CRC64;
Query Match 50.4%; Score 57; DB 2; Length 395;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 KRMSLAALAAALTVAGAMLA 19
|||:||||:||||:|
Db 13 KRLKPLAAAVAGVLLA 30
|||:||||:||||:|
RESULT 5
Q840C2 PRELIMINARY; PRT; 430 AA.
AC Q840C2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Endo-beta-1,4-mannanase 5A.
GN Name=Mann5A;
OS Cellvibrrio japonicus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Cellvibrrio.
OX NCBI_TaxID=155077;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22588103; PubMed=12523937;
RA Hogg D., Pell G., Dupree P., Goubet F., Martin-Orue S.M., Armand S.,
RA Gilbert H.J.;
RT "The modular architecture of Cellvibrrio japonicus mannanases in
RT glycoside hydrolase families 5 and 26 points to differences in their
RT role in mannan degradation.",
RL Biochem. J. 371:1027-1043(2003).
DR EMBL: AY187031; AAC01759.1; -
DR HSSP; P14768; IE8R.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl bonds; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR009031; CBDX.
DR InterPro: IPR002883; Dockerin_CBD_5.
DR Pfam: PF02013; CBM_10; 2.
DR Pfam: PF00150; Cellulase; 1.
DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; UNKNOWN 1.
SQ SEQUENCE 430 AA; 46325 MW; AEA56FBE0A9B073F CRC64;
Query Match 50.4%; Score 57; DB 2; Length 430;
Best Local Similarity 54.2%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 2 KRMSLAALAAALTVAGAMLAAPVATA 25
|||:||||:||||:|
Db 24 RRLKPLAAAVAGVLLA 47
|||:||||:||||:|
RESULT 6

Q7NXL7
ID Q7NXL7 PRELIMINARY; PRT; 346 AA.
AC Q7NXL7
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Peptidoglycan N-acetylmuramoylhydrolase (EC 3.2.1.17).
GN Name=mtB; OrderedLocusNames=CV1609;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Axaripe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Buriti H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasek T.B., Cunha-Junior N.C., Fagundes N., Falcão C.L.,
RA Fantinatti P., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furian L.R., T.B.,
RA Gazzinelli R.T., Gomes E.A., Gonçalves P.R., Grangiero T.B.,
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhão A.Q., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros R.B., Meissner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixão R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Rondinelli E.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT remarkable and exploitable bacterial adaptability.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
DR EMBL: AS016915; A059285.1; --
DR GO: GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO: GO:0003796; F:lysozyme activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR KW Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 346 AA; 38077 MW; EFC9818C37B1B712 CRC64;
Query Match 49.6%; Score 56; DB 2; Length 346;
Best Local Similarity 56.0%; Pred. No. 20;
Matches 14; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 1 MKRMSLAAALTVAGMLAAPVATA 25
Db 1 MKSMLKIAAALAGALTAPPAQA 25
RESULT 7
Q6SH08 PRELIMINARY; PRT; 438 AA.
ID Q6SH08
AC Q6SH08
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Vanillate transporter Vank, Putative.
GN ORFNames=EBAC000-65D02.5;
OS uncultured bacterium 443.
OC Bacteria; environmental samples.
OX NCBI_TaxID=257393;
RN [1]

RP SEQUENCE FROM N.A.
RA DeLong E.F.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Heidelberg J.F., Eisen J.A., Nelson W.C., DeLong E.F.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL: AY458640; AAR37811.1; --
DR InterPro: IPR007114; MFS.
DR InterPro: IPR005828; Sub-transporter.
DR InterPro: IPR005829; Sug-transporter.
DR Pfam: PF00083; Sugar tr; 1.
DR PROSITE: PS00850; MFS; 1.
DR PROSITE: PS00246; SUGAR_TRANSPORT_1; UNKNOWN 1.
DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN 1.
KW Transmembrane.
SQ SEQUENCE 438 AA; 46581 MW; D61B2769CD387C0F CRC64;
Query Match 47.8%; Score 54; DB 2; Length 438;
Best Local Similarity 51.9%; Pred. No. 45;
Matches 14; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
QY 3 RMKSLAAALTV----AGMLAAPVATA 25
Db 144 RFKSLAVSLVVMGYPGAILAGPMANA 170
RESULT 8
AAR37811 PRELIMINARY; PRT; 438 AA.
ID AAR37811
AC AAR37811
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Vanillate transporter Vank, Putative.
GN EBAC000-65D02.5.
OS uncultured bacterium 443.
OC Bacteria; environmental samples.
OX NCBI_TaxID=257393;
RN [1]
RP SEQUENCE FROM N.A.
RA DeLong E.F.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Heidelberg J.F., Eisen J.A., Nelson W.C., DeLong E.F.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY458640; AAR37811.1; --
SQ SEQUENCE 438 AA; 46581 MW; D61B2769CD387C0F CRC64;
Query Match 47.8%; Score 54; DB 2; Length 438;
Best Local Similarity 51.9%; Pred. No. 45;
Matches 14; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
QY 3 RMKSLAAALTV----AGMLAAPVATA 25
Db 144 RFKSLAVSLVVMGYPGAILAGPMANA 170
RESULT 9
Q716L8 PRELIMINARY; PRT; 122 AA.
ID Q716L8
AC Q716L8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Qp57.
OS Mycobacteriophage PGI.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=213236;

RN SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082336; PubMed=11214974;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idehara K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti (supplement).";
 RL DNA Res. 7:381-406(2000).
 DR EMBL; AP003012; BAB54123.1; -;
 DR HSSP; P02917; 2LIV.
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact...; IEA.
 DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
 DR GO; GO:0006865; P:amino acid transport; IEA.
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000709; Leu_ile_Val_bind.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR PRINTS; PR00337; LEUILEVALBP.
 KW Complete proteome.
 SQ SEQUENCE 399 AA; 42203 MW; CCD47F16F1F6C3 CRC64;

 Query Match 46.0%; Score 52; DB 2; Length 399;
 Best Local Similarity 52.0%; Pred. No. 79;
 Matches 13; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

 QY 1 MKRMKSLAAALTAVAGMLAAPVATA 25
 DB 27 MKKMSILSAA--IFGLMMSAPVAPA 49

 RESULT 16
 Q93HK7
 ID Q93HK7 PRELIMINARY; PRT; 87 AA.
 AC Q93HK7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putative secreted protein.
 GN OrderedLocusNames=SAV5360;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=21477403; PubMed=11572948;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis; deducing the ability of producing secondary
 RT metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis.";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL; AB070939; BAB69180.1; -;
 DR EMBL; AP005042; BAB73072.1; -;
 KW Complete proteome.
 SQ SEQUENCE 87 AA; 8292 MW; 72F118A11C5258E5 CRC64;

 Query Match 45.6%; Score 51.5; DB 2; Length 87;
 Best Local Similarity 65.2%; Pred. No. 28;
 Matches 13; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Matches 15; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

 QY 4 MKSLAAALTAVAGMLAAPVATA 25
 DB 1 MKSLAAAVVAGSMVLAVGAVAPA 23

 RESULT 17
 Q8KQL9
 ID Q8KQL9 PRELIMINARY; PRT; 948 AA.
 AC Q8KQL9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ORF.
 OS Saccharopolyspora erythraea (Streptomyces erythraeus).
 OC Bacteria; Actinobacteridae; Actinobacteriales; Actinomycetales;
 OC Pseudonocardiales; Pseudonocardaceae; Saccharopolyspora.
 OX NCBI_TaxID=1836;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22025301; PubMed=12028378;
 RA Cortes J., Velasco J., Foster G., Blackaby A.P., Rudd B.A.,
 RA Wilkinson B.;
 RT "Identification and cloning of a type III polyketide synthase required
 RT for diffusible pigment biosynthesis in Saccharopolyspora erythraea.";
 RL Mol. Microbiol. 44:1213-1224(2002).
 DR EMBL; AV078067; AAL78057.1; -;
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0017000; P:antibiotic biosynthesis; IEA.
 DR InterPro; IPR02692; Peptidase S45.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF01804; Penicillin_amidase; 1.
 DR PROSITE; PS00030; RRM_ENP_1; UNKNOWN 1.
 SQ SEQUENCE 948 AA; 102156 MW; AD69234AF2ACD093 CRC64;

 Query Match 45.6%; Score 51.5; DB 2; Length 948;
 Best Local Similarity 46.4%; Pred. No. 1.8e+02;
 Matches 13; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

 QY 1 MKRMKSLAAALT--VAGMLAAPVATA 25
 DB 1 MSRLQRLVAALSAGAVVGSLLIAPASTA 28

 RESULT 18
 Q8NR31
 ID Q8NR31 PRELIMINARY; PRT; 104 AA.
 AC Q8NR31; Q6MSV1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical membrane protein (Putative secreted protein).
 GN OrderedLocusNames=Cgl1233, cgl1389;
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteridae; Actinobacteriales; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RX PubMed=12948626;
 RA Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
 RA Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
 RA Gessmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
 RA McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Pühler A.,
 RA Rey D.A., Ruckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I.,

DR PIR: G70587; G70587.
 DR TIGR; NT2445; -.
 DR Tuberculin; RV2376C; -.
 KW Antigen; Complete proteome; Direct protein sequencing; Signal.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 48
 FT CHAIN 49 168 Low molecular weight antigen MTB12.
 FT CONFLICT 142 142 Q -> R (in Ref. 3).
 SQ SEQUENCE 168 AA; 16635 MW; A809937458009BFD CRC64;

Query Match 45.1%; Score 51; DB 1; Length 168;
 Best Local Similarity 60.0%; Pred. No. 55;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTVAGMLAA 20
 DB 1 MKRMKSLAAALTVAGMLAA 20

RESULT 21
 Q8XVA4 PRELIMINARY; PRT; 248 AA.
 AC Q8XVA4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE PUTATIVE CYTOCHROME C1 TRANSMEMBRANE PROTEIN.
 GN Name=petC; Synonyms=RS00164; OrderedLocusNames=RS02927;
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GMI1000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Siquier P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646072; CAD16634.1; -.
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000345; CytC_heme_B5.
 DR InterPro; IPR009056; Cytochrome_C.
 DR InterPro; IPR002326; Cyt_C1.
 DR Pfam; PF02167; Cytochrom_C1; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
 SK Complete proteome; Transmembrane.
 SQ SEQUENCE 248 AA; 28276 MW; 06418B0ADDE5C05EE CRC64;

Query Match 45.1%; Score 51; DB 2; Length 248;
 Best Local Similarity 57.9%; Pred. No. 75;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 MKSLAAALTVAGMLAAPV 22
 DB 1 MKSLAAALTVAGMLAAPV 19

RESULT 22
 Q9S3L6 PRELIMINARY; PRT; 431 AA.
 AC Q9S3L6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative 36kDa protease.

OS Bacillus sphaericus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1421;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2297;
 RX MEDLINE=99318657; PubMed=10388698;
 RA Servant P., Rosso M.L., Hamon S., Poncet S., Delecluse A.,
 RA Rapoport G.;
 RT "Production of CryIIA and CryIIb toxins in Bacillus sphaericus
 RT confers toxicity towards Aedes aegypti and resistant Culex
 RT populations.";
 RL Appl. Environ. Microbiol. 65:3021-3026(1999).
 CC -1- SIMILARITY: Belongs to peptidase family S8.
 DR EMBL; AJ238598; CAB46075.1; -.
 DR FDB; 1EA7; X-ray; A=122-431.
 DR MEROPS; S08.113; -.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004289; F:subtilase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000209; Pept_S8_S53.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1.
 DR PROSITE; PS00137; SUBTILASE HIS; 1.
 DR PROSITE; PS00138; SUBTILASE SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 431 AA; 45345 MW; C1CFEA8E71C2C6D2 CRC64;

Query Match 45.1%; Score 51; DB 2; Length 431;
 Best Local Similarity 44.0%; Pred. No. 1.1e+02;
 Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTVAGMLAAPVATA 25
 DB 1 MKRMKSLAAALTVAGMLAAPVATA 25

RESULT 23
 Q54327 PRELIMINARY; PRT; 434 AA.
 AC Q54327;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Toxin degrading protease.
 OS Bacillus sphaericus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1421;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SSII-1;
 RA Wati M.R., Thanabalu T., Porter A.G.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family S8.
 DR EMBL; U32628; AAB93489.1; -.
 DR HSSP; Q9S3L6; 1EA7.
 DR MEROPS; S08.113; -.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004289; F:subtilase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000209; Pept_S8_S53.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1.
 DR PROSITE; PS00137; SUBTILASE HIS; 1.
 DR PROSITE; PS00138; SUBTILASE SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 434 AA; 45773 MW; C97A00965AAE7943 CRC64;

Query Match 45.1%; Score 51; DB 2; Length 434;
 Best Local Similarity 44.0%; Pred. No. 1.2e+02;
 Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;


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QY 1 MKRMSLAALTVAGAMLAAPVATA 25
  ||||| : |||: |||
Db 4 MKRMSLTLISLIAGSVINPVATA 28
  ||||| : |||: |||

RESULT 24
Q8XTE9 PRELIMINARY; PRT; 482 AA.
ID Q8XTE9
AC Q8XTE9
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE PROBABLE TRANSMEMBRANE PROTEIN.
GN Name-RS95514; OrderedLocusNames=RS9p164;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]_TaxID=305;
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11923852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502 (2002).
RL EMBL; AL646076; CAD17315.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0015297; F:antipporter activity; IEA.
DR GO; GO:0015238; F:drug transporter activity; IEA.
DR GO; GO:0006855; P:multidrug transport; IEA.
DR InterPro; IPR002528; Mate.
DR Pfam; PF01554; Mate; 2.
DR TIGRFAMs; TIGR00797; mate; 1.
KW Complete proteome; Plasmid; Transmembrane.
SQ SEQUENCE 482 AA; 50177 MW; 85A3F26DAB39D00F CRC64;

Query Match 45.1%; Score 51; DB 2; Length 482;
Best Local Similarity 58.8%; Pred. No. 1.2e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 LAAALTVAGAMLAAPVA 23
  ||||| : |||: |||
Db 111 LAVLIALAGAMLAGPIA 127
  ||||| : |||: |||

RESULT 25
Q7W382 PRELIMINARY; PRT; 328 AA.
ID Q7W382
AC Q7W382
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Metallo-beta-lactamase superfamily protein.
GN OrderedLocusNames=Bpp4164;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]_TaxID=519;
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin M., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40 (2003).
RL EMBL; BX640451; CAE34996.1; -.
DR InterPro; IPR001279; Blactmase-like.
DR Pfam; PF00753; Lactamase_B; 1.
KW Complete proteome.
SQ SEQUENCE 328 AA; 34864 MW; E410012E8F0F1A93 CRC64;

Query Match 44.7%; Score 50.5; DB 2; Length 328;
Best Local Similarity 56.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

QY 3 RMKSLAALTVAG---AMLAAPVAT 24
  ||||| : |||: |||
Db 9 RRLAALAAALTAAGVQPALATAPVLT 33
  ||||| : |||: |||

RESULT 26
Q7WEK1 PRELIMINARY; PRT; 328 AA.
ID Q7WEK1
AC Q7WEK1
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Metallo-beta-lactamase superfamily protein.
GN OrderedLocusNames=BB4634;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]_TaxID=518;
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin M., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40 (2003).
RL EMBL; BX640451; CAE34996.1; -.
DR InterPro; IPR001279; Blactmase-like.
DR Pfam; PF00753; Lactamase_B; 1.
KW Complete proteome.
SQ SEQUENCE 328 AA; 34864 MW; E410012E8F0F1A93 CRC64;

Query Match 44.7%; Score 50.5; DB 2; Length 328;
Best Local Similarity 56.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

QY 3 RMKSLAALTVAG---AMLAAPVAT 24
  ||||| : |||: |||
Db 9 RRLAALAAALTAAGVQPALATAPVLT 33
  ||||| : |||: |||

RESULT 27
Q829D3 PRELIMINARY; PRT; 81 AA.
ID Q829D3
AC Q829D3;
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DR EMBL; AL939113; CAB92269.1; -.
KW Complete proteome.
SQ SEQUENCE 100 AA; 9870 MW; 0D770ED1D46F938A CRC64;

Query Match 44.2%; Score 50; DB 2; Length 100;
Best Local Similarity 64.7%; Pred. No. 50;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 MKSLAAALTAVAGMLAA 20
Db 1 MKSLKRAAVVAGSLVAA 17

RESULT 29
RL7 RICPR STANDARD; PRT; 125 AA.
AC Q9E21.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 50S ribosomal protein L7/L12.
GN Name=rpL7; OrderedLocusNames=RP139;
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsia;
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893; DOI=10.1038/24094;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sicheritz-Ponten T., Almark U.C.M., Podowski J.R., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
CC -!- FUNCTION: Seems to be the binding site for several of the factors
CC involved in protein synthesis and appears to be essential for
CC accurate translation (by similarity).
CC -!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AJ235270; CAA14607.1; -.
DR PIR; H71723; H71723.
DR HSSP; P29396; 1DD3.
DR HAWAP; MP_00368; -.
DR InterPro; IPR000206; Ribosomal_L12.
DR InterPro; IPR008932; Ribosomal_L12/7.
DR Pfam; PF00542; Ribosomal_L12; 1.
DR ProDom; PD001326; Ribosomal_L12; 1.
DR TIGRfams; TIGR00855; L12; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 125 AA; 13213 MW; 431EDA82F25DB867 CRC64;

Query Match 44.2%; Score 50; DB 1; Length 125;
Best Local Similarity 60.0%; Pred. No. 60;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 6 SLAAALTAVAGMLAAAPVATA 25
Db 33 SAAAPITVAGVAAPLAAE 52

RESULT 30
Q8NTB4 PRELIMINARY; PRT; 279 AA.
ID Q8NTB4
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AC Q8NTB4: Q6M7W9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical membrane protein (Conserved secreted protein).
GN OrderedLocusNames=Cg10393, cg0471;
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX PubMed=12948626;
RA Kallinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
RA Burkowski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
RA Goemann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
RA McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Puehler A.,
RA Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I.,
RA Tauch A.;
RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence
RT and its impact on the production of L-aspartate-derived amino acids
RT and vitamins";
RL J. Biotechnol. 104:5-25(2003).
DR EMBL; AF005275; BAB97786.1; -.
DR EMBL; BX927149; CAF19108.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 279 AA; 29006 MW; AA5BCD021149FD2E CRC64;

Query Match 44.2%; Score 50; DB 2; Length 279;
Best Local Similarity 48.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAAPVATA 25
Db 1 MNRFPSSALLAASVAGAALAIPATSA 25

RESULT 31
ID CAF19108 PRELIMINARY; PRT; 279 AA.
AC CAF19108;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Conserved secreted protein.
GN CG0471.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX PubMed=12948626;
RA Kallinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
RA Burkowski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
RA Goemann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
RA McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Puehler A.,
RA Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I.,
RA Tauch A.;
RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence
RT and its impact on the production of L-aspartate-derived amino acids
RT and vitamins";
RL J. Biotechnol. 104:5-25(2003).
DR EMBL; BX927149; CAF19108.1; -.
SQ SEQUENCE 279 AA; 29006 MW; AA5BCD021149FD2E CRC64;

Query Match 44.2%; Score 50; DB 2; Length 279;
Best Local Similarity 48.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAAPVATA 25
Db 1 MNRFPSSALLAASVAGAALAIPATSA 25

RESULT 32
ID Q92MJ0 PRELIMINARY; PRT; 284 AA.
AC Q92MJ0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE OUTER MEMBRANE PROTEIN.
GN OrderedLocusNames=R02626; ORFNames=Smc02451;
OS Rhizobium meliloti (Sinorhizobium meliloti);
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21368234; PubMed=11474104;
RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kaiman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
RA Ransperger U., Surzycki R., Thebault P., Vandenbol M.,
RA Vorholter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti";
RL Science 293:668-672(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ransperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -1- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.
DR EMBL; AL591731; CAC47205.1; -.
DR HSSP; P21202; 1M5Y.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR00297; Rotamase.
DR Pfam; PF00639; Rotamase.
DR PROSITE; PS0198; PPI_C/PP1ASE_2; 1.
KW Complete proteome; Isomerase; Rotamase.
SQ SEQUENCE 284 AA; 31460 MW; 700277987D225C53 CRC64;

Query Match 44.2%; Score 50; DB 2; Length 284;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 MKRMKSLAAALTAVAGAMLAAPVATA 25
Db 1 MSRYKTLAAALV--AMTAAAGVAA 23

RESULT 33

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Q6W1L8
ID Q6W1L8; PRELIMINARY; PRT; 353 AA.
AC Q6W1L8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE D-ribose-binding protein.
GN ORFNames=NRGR10102;
OS Rhizobium sp. (strain NGR234).
OG Plasmid megaplasmid 2.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGR234;
RA Broughton W.J., Perret X., Staehelin C., Schmitz R.A., Raasch C.,
RA Liesegang H., Gottschalk G., Streit W.R.;
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY316747; AAQ87350.1; -.
KW Plasmid.
SQ SEQUENCE 353 AA; 37024 MW; 2C976A4D4EA37839 CRC64;

Query Match 44.2%; Score 50; DB 2; Length 353;
Best Local Similarity 48.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

Qy 1 MKRMKSLAALTVAG--AMLAAPVA 23
Db 1 MRKFSLKSLSLASLALAAAPAA 25

RESULT 34
AAQ87350 PRELIMINARY; PRT; 353 AA.
AC AAQ87350;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE D-ribose-binding protein.
GN NGR10102.
OS Rhizobium sp. (strain NGR234).
OG Plasmid megaplasmid 2.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGR234;
RA Broughton W.J., Perret X., Staehelin C., Schmitz R.A., Raasch C.,
RA Liesegang H., Gottschalk G., Streit W.R.;
RA "Comparative DNA analysis of two large contigs of the Rhizobium sp.
RT NGR234 megaplasmid 2.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY316747; AAQ87350.1; -.
KW Plasmid.
SQ SEQUENCE 353 AA; 37024 MW; 2C976A4D4EA37839 CRC64;

Query Match 44.2%; Score 50; DB 2; Length 353;
Best Local Similarity 48.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

Qy 1 MKRMKSLAALTVAG--AMLAAPVA 23
Db 1 MRKFSLKSLSLASLALAAAPAA 25

RESULT 35
Q9L0G9 PRELIMINARY; PRT; 431 AA.
ID Q9L0G9
AC Q9L0G9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative ntegral membrane protein.
GN OrderedLocusNames=SCO4788; ORFNames=SCD63.20;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RC MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RX Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939121; CAB82027.1; -.
KW Complete proteome.
SQ SEQUENCE 431 AA; 44610 MW; 049C7148CF41ASE5 CRC64;

Query Match 44.2%; Score 50; DB 2; Length 431;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 RMKSLAALTVAGMLAA 20
Db 131 RTAGLAALVVAGALTA 148

RESULT 36
Q8XTF1 PRELIMINARY; PRT; 517 AA.
ID Q8XTF1
AC Q8XTF1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE TRANSMEMBRANE PROTEIN.
GN Name=RS05517; OrderedLocusNames=RS0161;
CS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billaut A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunha S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schliex T.,
RA Siquier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646076; CAD17312.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR009199; PqAA.
DR PIRSF; PIRSF014728; PqAA.
KW Complete proteome; Plasmid; Transmembrane.
SQ SEQUENCE 517 AA; 56203 MW; 151E4DF95FEF5A63 CRC64;

Query Match 44.2%; Score 50; DB 2; Length 517;
Best Local Similarity 45.8%; Pred. No. 1.8e+02;
Matches 11; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

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QY 2 KMKSLAALATVAGAMLAAPVATA 25
 : : : : :
 Db 21 RMWKRLVANTLTAUACPLALA 44

RESULT 37

Q73W90 PRELIMINARY; PRT; 185 AA.
 AC Q73W90;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=MAP2770;
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
 OC Mycobacterium avium complex (MAC).
 OX NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=k10;
 RA Li L., Bannantine J., Zhang Q., Anonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 RE EMBL; AB017237; AAS05087.1;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 185 AA; 19316 MW; 3E4D53FBB0851873 CRC64;

Query Match 43.8%; Score 49.5; DB 2; Length 185;
 Best Local Similarity 60.9%; Pred. No. 95;
 Matches 14; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 3 RMKSLAALATVAGAMLAAPVATA 25
 : : : : :
 Db 12 RMSTLAALAT-ACLTAPGATA 33

RESULT 38

AAS05087 PRELIMINARY; PRT; 185 AA.
 AC AAS05087;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN MAP2770.
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=k10;
 RA Li L., Bannantine J., Zhang Q., Anonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 RE EMBL; AB017237; AAS05087.1;
 KW Hypothetical protein.
 SQ SEQUENCE 185 AA; 19316 MW; 3E4D53FBB0851873 CRC64;

Query Match 43.8%; Score 49.5; DB 2; Length 185;
 Best Local Similarity 60.9%; Pred. No. 95;
 Matches 14; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 3 RMKSLAALATVAGAMLAAPVATA 25
 : : : : :
 Db 12 RMSTLAALAT-ACLTAPGATA 33

RESULT 39

Q9X922 PRELIMINARY; PRT; 82 AA.
 AC Q9X922;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative small secreted protein.
 GN OrderedLocusNames=SCO1800; ORFNames=SCI5.08c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AS(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL599110; CAB45292.1;
 DR PIR; T36861; T36861.
 DR InterPro; IPR005528; DUF320.
 DR Pfam; PF03777; DUF320; 1.
 KW Complete proteome.
 SQ SEQUENCE 82 AA; 7760 MW; 0400569E5A7E097C CRC64;

Query Match 43.4%; Score 49; DB 2; Length 82;
 Best Local Similarity 44.0%; Pred. No. 59;
 Matches 11; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 MKRMKSLAALATVAGAMLAAPVATA 25
 : : : : :
 Db 1 MNLKKAAAVTMVAGLIAAGAWA 25

RESULT 40

Q6N1M5 PRELIMINARY; PRT; 231 AA.
 AC Q6N1M5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ribonuclease T2 precursor.
 GN OrderedLocusNames=RPA4380;
 OS Rhodopseudomonas palustris.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_TaxID=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., C.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 photosynthetic bacterium Rhodopseudomonas palustris.";
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL; BX572607; CAE29821.1;
 DR InterPro; IPR001568; RNase_T2.
 DR Pfam; PF00445; Ribonuclease_T2; 1.
 DR PROSITE; PS00530; RNase_T2_1; 1.
 KW Complete proteome; Signal.
 FT SIGNAL 1 28 Potential.
 SQ SEQUENCE 231 AA; 26028 MW; BC5AE77C44AA6624 CRC64;

Query Match 43.4%; Score 49; DB 2; Length 231;

Best Local Similarity 45.8%; Pred. No. 1.3e+02;
Matches 11; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 2 KRKSLAAALTIVAGAMLAAPVATA 25
Db 6 RRRSLIAACAVVGALFTSAVAEA 29

Search completed: December 1, 2004, 11:50:12
Job time : 192 secs

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OM protein - protein search, using sw model

Run on: December 1, 2004, 11:41:50 ; Search time 37 seconds
(without alignments)
44.809 Million cell updates/sec

Title: US-10-673-860-3

Perfect score: 113

Sequence: 1 MKRMKSLAAALTVAGMLAAPVATA 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/1aa/5A-COMB.pep:*

2: /cgn2_6/prodata/1/1aa/5B-COMB.pep:*

3: /cgn2_6/prodata/1/1aa/6A-COMB.pep:*

4: /cgn2_6/prodata/1/1aa/6B-COMB.pep:*

5: /cgn2_6/prodata/1/1aa/PCITUS-COMB.pep:*

6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	45.1	107	3	US-08-818-112-83
2	51	45.1	107	3	US-08-818-111-84
3	51	45.1	107	3	US-09-056-556-83
4	51	45.1	107	4	US-09-072-596-84
5	51	45.1	107	4	US-09-072-967-83
6	51	45.1	168	3	US-08-818-112-100
7	51	45.1	168	3	US-08-818-111-95
8	51	45.1	168	3	US-09-056-556-100
9	51	45.1	168	4	US-09-072-596-95
10	51	45.1	168	4	US-09-072-967-100
11	51	45.1	187	3	US-08-818-112-63
12	51	45.1	187	3	US-08-818-111-64
13	51	45.1	187	3	US-09-056-556-63
14	51	45.1	187	4	US-09-072-596-64
15	51	45.1	187	4	US-09-072-967-63
16	45	40.7	470	4	US-09-328-352-5397
17	45	39.8	229	4	US-09-270-767-40998
18	45	39.8	229	4	US-09-270-767-56214
19	45	39.8	322	4	US-09-489-039A-9408
20	45	39.8	563	3	US-08-362-525-12
21	45	39.8	659	3	US-08-894-818B-1
22	45	39.8	659	4	US-09-445-472-12
23	45	39.8	659	4	US-10-030-624-12
24	45	39.8	1264	4	US-09-252-991A-30264
25	44.5	39.4	191	4	US-09-270-767-35822
26	44.5	39.4	191	4	US-09-270-767-50839
27	44.5	39.4	303	3	US-09-159-106-13

28	44.5	39.4	435	3	US-09-159-106-11	Sequence 11, Appl
29	44	38.9	253	4	US-09-154-750A-83	Sequence 83, Appl
30	44	38.9	255	4	US-09-489-039A-10395	Sequence 10395, A
31	44	38.9	284	4	US-09-583-110-4830	Sequence 4830, Ap
32	44	38.9	356	4	US-09-252-991A-25482	Sequence 25482, A
33	44	38.9	415	4	US-09-252-991A-27669	Sequence 27669, A
34	44	38.9	442	4	US-09-252-991A-25257	Sequence 25257, A
35	44	38.9	681	4	US-09-252-991A-24159	Sequence 24159, A
36	43.5	38.5	30	3	US-09-105-390-22	Sequence 22, Appl
37	43	38.1	187	6	5217891-4	Patent No. 5217891
38	43	38.1	190	4	US-09-270-767-32610	Sequence 32610, A
39	43	38.1	190	4	US-09-270-767-47827	Sequence 47827, A
40	43	38.1	458	6	5217891-15	Patent No. 5217891
41	43	38.1	514	4	US-09-252-991A-25281	Sequence 25281, A
42	42.5	37.6	274	4	US-09-134-000C-3673	Sequence 3673, Ap
43	42.5	37.6	359	1	US-08-457-997B-2	Sequence 2, Appl
44	42.5	37.6	359	3	US-08-467-722A-2	Sequence 2, Appl
45	42.5	37.6	359	4	US-09-451-184-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-818-112-83
; Sequence 83, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, David C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,112
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-818-112-83

Query Match 45.1%; Score 51; DB 3; Length 107;
Best Local Similarity 60.0%; Pred. No. 1.7;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
| : : : : :
Db 10 MKMVKSLAAAGLTAAGAA 29

RESULT 2
US-08-818-111-84
; Sequence 84, Application US/08818111
; Patent No. 6338852
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonia
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,111
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-818-111-84

Query Match 45.1%; Score 51; DB 3; Length 107;
Best Local Similarity 60.0%; Pred. No. 1.7;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
| : : : : :
Db 10 MKMVKSLAAAGLTAAGAA 29

RESULT 3
US-09-056-556-83
; Sequence 83, Application US/09056556
; Patent No. 6350456
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle

TREATM

STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-83

Query Match 45.1%; Score 51; DB 3; Length 107;
Best Local Similarity 60.0%; Pred. No. 1.7;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
| : : : : :
Db 10 MKMVKSLAAAGLTAAGAA 29

RESULT 4
US-09-072-596-84
; Sequence 84, Application US/09072596
; Patent No. 6458366
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonia
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,596
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C9
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-072-596-84
Query Match 45.1%; Score 51; DB 4; Length 107;
Best Local Similarity 60.0%; Pred. No. 1.7;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 MKRMKSLAALTVAGAMLAA 20
DB 10 MKRMKSLAAGLTAAAAIGAA 29
RESULT 5
US-09-072-967-83
Sequence 83, Application US/09072967
Patent No. 6592877
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-072-967-83
Query Match 45.1%; Score 51; DB 4; Length 107;
Best Local Similarity 60.0%; Pred. No. 1.7;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 MKRMKSLAALTVAGAMLAA 20

DB 10 MKRMKSLAAGLTAAAAIGAA 29
RESULT 6
US-08-818-112-100
Sequence 100, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-112-100
Query Match 45.1%; Score 51; DB 3; Length 168;
Best Local Similarity 60.0%; Pred. No. 2.9;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 MKRMKSLAALTVAGAMLAA 20
DB 1 MKRMKSLAAGLTAAAAIGAA 20
RESULT 7
US-08-818-111-95
Sequence 95, Application US/08818111
Patent No. 6338852
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/818,111
 ; FILING DATE: 13-MAR-1997
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Maki, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.417C6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 95:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 168 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-818-111-95

Query Match 45.1%; Score 51; DB 3; Length 168;
 Best Local Similarity 60.0%; Pred. No. 2.9;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKMKSLAAALTAVAGAMLAA 20
 DB 1 MKMKSLAAALTAVAGAMLAA 20

RESULT 8
 US-09-056-556-100
 ; Sequence 100, Application US/09056556
 ; Patent No. 6350456
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Dillon, Davin C.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
 ; NUMBER OF SEQUENCES: 241
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/056,556
 ; FILING DATE: 07-APR-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Maki, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.457
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 100:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 168 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-056-556-100

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 168 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-056-556-100

Query Match 45.1%; Score 51; DB 3; Length 168;
 Best Local Similarity 60.0%; Pred. No. 2.9;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKMKSLAAALTAVAGAMLAA 20
 DB 1 MKMKSLAAALTAVAGAMLAA 20

RESULT 9
 US-09-072-596-95
 ; Sequence 95, Application US/09072596
 ; Patent No. 6458366
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Campos-Neto, Antonia
 ; APPLICANT: Houghton, Raymond
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Twardzik, Daniel R.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Hendrickson, Ronald C.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
 ; NUMBER OF SEQUENCES: 350
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/072,596
 ; FILING DATE: 05-MAY-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Maki, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.417C9
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 95:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 168 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-072-596-95

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 168 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-072-596-95

Query Match 45.1%; Score 51; DB 4; Length 168;
 Best Local Similarity 60.0%; Pred. No. 2.9;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKMKSLAAALTAVAGAMLAA 20
 DB 1 MKMKSLAAALTAVAGAMLAA 20

RESULT 10

US-09-072-967-100
; Sequence 100, Application US/09072967
; Patent No. 6592877
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-072-967-100
Query Match 45.1%; Score 51; DB 4; Length 168;
Best Local Similarity 60.0%; Pred. No. 2.9;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MKMKSLAALTVAGAMLAA 20
Db 1 MKMKSLAALTVAGAMLAA 20
RESULT 11
US-08-818-112-63
; Sequence 63, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
US-08-818-111-64
; Sequence 64, Application US/08818111
; Patent No. 6338852
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-818-112-63
Query Match 45.1%; Score 51; DB 3; Length 187;
Best Local Similarity 60.0%; Pred. No. 3.2;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MKMKSLAALTVAGAMLAA 20
Db 20 MKMKSLAALTVAGAMLAA 39
RESULT 12
US-08-818-111-64
; Sequence 64, Application US/08818111
; Patent No. 6338852
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-818-112-63

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; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-818-111-64

Query Match 45.1%; Score 51; DB 3; Length 187;
Best Local Similarity 60.0%; Pred. No. 3.2;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
Db 20 MKMKVSIAGLTAAGAAIGAA 39

RESULT 13
US-09-056-556-63
; Sequence 63, Application US/09056556
; Patent No. 6350456
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,556
; FILING DATE: 07-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.457
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-056-556-63

Query Match 45.1%; Score 51; DB 3; Length 187;
Best Local Similarity 60.0%; Pred. No. 3.2;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
Db 20 MKMKVSIAGLTAAGAAIGAA 39

RESULT 14
US-09-072-596-64
; Sequence 64, Application US/09072596
; Patent No. 6458366
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle

; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,596
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-072-596-64

Query Match 45.1%; Score 51; DB 4; Length 187;
Best Local Similarity 60.0%; Pred. No. 3.2;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
Db 20 MKMKVSIAGLTAAGAAIGAA 39

RESULT 15
US-09-072-967-63
; Sequence 63, Application US/09072967
; Patent No. 6592877
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
```

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; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,967
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-072-967-63

Query Match 45.1%; Score 51; DB 4; Length 187;
Best Local Similarity 60.0%; Pred. No. 3.2;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRKSLAAALTAVAGAMLAAPVATA 20
Db 20 MKMKVKSIAAGLTAAAGTA 39

RESULT 16
US-09-328-352-5397
; Sequence 5397, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5397
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5397

Query Match 40.7%; Score 46; DB 4; Length 470;
Best Local Similarity 43.5%; Pred. No. 51;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 3 RMKSLAAALTAVAGAMLAAPVATA 25
Db 5 RMKMKVKSIAAGLTAAAGTA 27

RESULT 17
US-09-270-767-40998
; Sequence 40998, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
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; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 40998
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-40998

Query Match 39.8%; Score 45; DB 4; Length 229;
Best Local Similarity 42.9%; Pred. No. 32;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 MKSLAAALTAVAGAMLAAPVAT 24
Db 207 VKSMKKISAAGDQVLAPVVT 227

RESULT 18
US-09-270-767-56214
; Sequence 56214, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 56214
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56214

Query Match 39.8%; Score 45; DB 4; Length 229;
Best Local Similarity 42.9%; Pred. No. 32;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 MKSLAAALTAVAGAMLAAPVAT 24
Db 207 VKSMKKISAAGDQVLAPVVT 227

RESULT 19
US-09-489-039A-9408
; Sequence 9408, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9408
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9408

Query Match 39.8%; Score 45; DB 4; Length 322;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKRKSLAAALTAVAGAMLA 20
Db 25 MKRLKYLSTLLVAVALIA 44
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RESULT 20

US-08-362-525-12
; Sequence 12, Application US/08362525
; Patent No. 6027910
; GENERAL INFORMATION:
; APPLICANT: KLIS, FRANCISCUS M.
; APPLICANT: SCHREUDER, MAARTEN P.
; APPLICANT: TOSCHKA, HOLSER Y.
; APPLICANT: VERRIPS, CORNELIS T.
; TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE
; TITLE OF INVENTION: CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,525
; FILING DATE: 04-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92202080.5
; FILING DATE: 08-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92203899.7
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/01763
; FILING DATE: 07-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 213289/T7020 (V)
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 563 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-362-525-12

Query Match 39.8%; Score 45; DB 3; Length 563;
Best Local Similarity 58.8%; Pred. No. 88;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 7 LAALTVAGAWLAAPVA 23
Db 8 LAALNVLVGLAQAPTA 24

RESULT 21

US-08-894-818B-1
; Sequence 1, Application US/08894818B
; Patent No. 6261822
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Hikaru
; APPLICANT: MORISHITA, Mio
; APPLICANT: YANAMOTO, Katsuhiko
; APPLICANT: MITTA, Masanori
; APPLICANT: ASADA, Kiyozo

APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TAKAKURA=1
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-818B-1

Query Match 39.8%; Score 45; DB 3; Length 659;
Best Local Similarity 46.2%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

QY 1 MKRMKSLAALT---VAGAWLAAPV 22
Db 1 MKRLGAVLVLLVGLLAGTALAAPV 26

RESULT 22

US-09-445-472-12
; Sequence 12, Application US/09445472
; Patent No. 6358726
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Hikaru
; APPLICANT: MORISHITA, Mio
; APPLICANT: SHIMOJO, Tomoko
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
; FILE REFERENCE: TAKAKURA=6
; CURRENT APPLICATION NUMBER: US/09/445,472
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 151969/1997
; PRIOR FILING DATE: 1997-06-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 12
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Thermococcus celer

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US-09-445-472-12
Query Match      39.8%; Score 45; DB 3; Length 659;
Best Local Similarity 46.2%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

QY 1 MKRMSLAALT- ---VAGMLAAPV 22
    |||: : : |||: : : |||: |||
Db 1 MKRLGAVLVLVGLLGTALAAPV 26

RESULT 23
US-10-090-624-12
; Sequence 12, Application US/10090624
; Patent No. 6783970
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Hikaru
; APPLICANT: MORISHITA, Mio
; APPLICANT: SHIMOJO, Tomoko
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
; FILE REFERENCE: TAKAKURA=6
; CURRENT APPLICATION NUMBER: US/10/090,624
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 09/445,472
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 151969/1997
; PRIOR FILING DATE: 1997-06-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 12
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Thermococcus celer
US-10-090-624-12

Query Match      39.8%; Score 45; DB 4; Length 659;
Best Local Similarity 46.2%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

QY 1 MKRMSLAALT- ---VAGMLAAPV 22
    |||: : : |||: : : |||: |||
Db 1 MKRLGAVLVLVGLLGTALAAPV 26

RESULT 24
US-09-252-991A-30264
; Sequence 30264, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30264
; LENGTH: 1264
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30264

Query Match      39.8%; Score 45; DB 4; Length 1264;
Best Local Similarity 54.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 4 MKSLAALTIVAGMLAAPVATA 25
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Db 133 MQSLAVELNLEGARLARQVADA 154
    |||: : : |||: : : |||: |||

RESULT 25
US-09-270-767-35622
; Sequence 35622, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 35622
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-35622

Query Match      39.4%; Score 44.5; DB 4; Length 191;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 14; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 7 LAAALTVA-GAMLAAPVATA 25
    |||: : : |||: : : |||: |||
Db 42 LAAPLAPAFAPLAAPVATA 61

RESULT 26
US-09-270-767-50839
; Sequence 50839, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 50839
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-50839

Query Match      39.4%; Score 44.5; DB 4; Length 191;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 14; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 7 LAAALTVA-GAMLAAPVATA 25
    |||: : : |||: : : |||: |||
Db 42 LAAPLAPAFAPLAAPVATA 61

RESULT 27
US-09-159-106-13
; Sequence 13, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
; APPLICANT: Ferrer, Pau
; APPLICANT: Diers, Ivan
; APPLICANT: Halkier, Torben
; APPLICANT: Hedegaard, Lisbeth
; TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
; FILE REFERENCE: 4693.204-US
; CURRENT APPLICATION NUMBER: US/09/159,106
; CURRENT FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0427/96

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; EARLIER FILING DATE: 1996-12-04
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: PCT/DK97/00160
; EARLIER FILING DATE: 1997-04-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-13

Query Match 39.4%; Score 44.5; DB 3; Length 303;
Best Local Similarity 56.5%; Pred. No. 53;
Matches 13; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

Qy 2 KRMS-LAAALTIVAGAMLAAPVA 23
Db 24 RLASALVAAALTAARAAALAVTVA 46

RESULT 28
US-09-159-106-11
; Sequence 11, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
; APPLICANT: Ferrer, Pau
; APPLICANT: Diers, Ivan
; APPLICANT: Halkier, Torben
; APPLICANT: Hedegaard, Lisbeth
; TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
; FILE REFERENCE: 4693.204-US
; CURRENT APPLICATION NUMBER: US/09/159,106
; CURRENT FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0427/96
; EARLIER FILING DATE: 1996-12-04
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: PCT/DK97/00160
; EARLIER FILING DATE: 1997-04-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11

Query Match 39.4%; Score 44.5; DB 3; Length 435;
Best Local Similarity 56.5%; Pred. No. 79;
Matches 13; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

Qy 2 KRMS-LAAALTIVAGAMLAAPVA 23
Db 24 RLASALVAAALTAARAAALAVTVA 46

RESULT 29
US-09-154-750A-83
; Sequence 83, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-154-750A-83

Query Match 38.9%; Score 44; DB 4; Length 253;
Best Local Similarity 76.9%; Pred. No. 51;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 AALTIVAGAMLAAP 21
Db 136 AALAVAGALEAAP 148

RESULT 30
US-09-489-039A-10395
; Sequence 10395, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10395
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10395

Query Match 38.9%; Score 44; DB 4; Length 255;
Best Local Similarity 40.0%; Pred. No. 52;
Matches 10; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MKRMKSIAAALTIVAGAMLAAPVATA 25
Db 4 MKLLKTPAAVMLAGGLFASVGAMA 28

RESULT 31
US-09-583-110-4830
; Sequence 4830, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4830
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4830

Query Match 38.9%; Score 44; DB 4; Length 284;


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Best Local Similarity 55.0%; Pred. No. 58;
Matches 11; Conservative 2; Mismatches 0; Gaps 0;

Qy 1 MKRMKSLAAALTAVAGAMLAA 20
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Db 3 IKKWLGLAALAVAGALAA 22

RESULT 32
US-09-252-991A-25482
; Sequence 25482, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25482
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25482

Query Match 38.9%; Score 44; DB 4; Length 356;
Best Local Similarity 56.2%; Pred. No. 75;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 9 AALTAVAGAMLAAAPVAT 24
   :|: ||| ||| ||| |||
Db 335 SAMTSGACRAAPIAT 350

RESULT 33
US-09-252-991A-27669
; Sequence 27669, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27669
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27669

Query Match 38.9%; Score 44; DB 4; Length 415;
Best Local Similarity 43.5%; Pred. No. 89;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTAVAGAMLAA 23
   :|: ||| ||| ||| |||
Db 203 LHLGVPVAPASAGQSLAAPA 225

RESULT 34
US-09-252-991A-25257
; Sequence 25257, Application US/09252991A
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Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25257
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25257

Query Match 38.9%; Score 44; DB 4; Length 442;
Best Local Similarity 47.8%; Pred. No. 95;
Matches 11; Conservative 6; Mismatches 4; Indels 2; Gaps 1;

Qy 3 RMKSLAAALTAVAGAMLAA 25
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Db 36 RLKAISIAL--AGSALVSPVAYA 56

RESULT 35
US-09-252-991A-24159
; Sequence 24159, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24159
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24159

Query Match 38.9%; Score 44; DB 4; Length 681;
Best Local Similarity 43.5%; Pred. No. 1.5e+02;
Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTAVAGAMLAA 23
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Db 264 LTRVGSLLASVRLAGALLAVGTA 286

RESULT 36
US-09-105-390-22
; Sequence 22, Application US/09105390
; Patent No. 6288303
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
; TITLE OF INVENTION: and Genes
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Denlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
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; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/09/105,390
; FILING DATE: Filled herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE: 25-JUN-97
; APPLICATION NUMBER: 60/050,675
; ATTORNEY/AGENT INFORMATION:
; NAME: Pettithory, Joanne R.
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 2000-0455.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-105-390-22

Query Match 38.1%; Score 43.5; DB 3; Length 30;
Best Local Similarity 39.3%; Pred. No. 5.6;
Matches 11; Conservative 6; Mismatches 8; Indels 3; Gaps 1;

QY 1 MKRMKSLAAALTVA---GAMLAAPVATA 25
| | | | | | | | | | | | | | | | | | | |
Db 1 MARRQGVASMLTIALIGAFASAPTSCTA 28

RESULT 37
5217891-4
; Patent No. 5217891
; APPLICANT: BRAKE, ANTHONY J.;VAN DEN BERG, JOHAN A.
; TITLE OF INVENTION: DNA CONSTRUCTS CONTAINING A KLUYVEROMYCES
; A FACTOR LEADER SEQUENCE FOR DIRECTING SECRETION OF HETEROLOGOUS
; POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/507,398
; FILING DATE: 09-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 78,551
; FILING DATE: 28-JUL-1987
; SEQ ID NO.4:
; LENGTH: 187
5217891-4

Query Match 38.1%; Score 43; DB 6; Length 187;
Best Local Similarity 41.7%; Pred. No. 52;
Matches 10; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTVA---GAMLAAPVAT 24
| | | | | | | | | | | | | | | | | | | |
Db 1 MKFSTILAAALTALISVVMAPVST 24

RESULT 38
US-09-270-767-32610
; Sequence 32610, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32610
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32610

Query Match 38.1%; Score 43; DB 4; Length 190;
Best Local Similarity 42.9%; Pred. No. 53;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTVA---GAMLAAP 21
| | | | | | | | | | | | | | | | | | | |
Db 7 IKRIAETAVAYAKAGAHIVAP 27

RESULT 39
US-09-270-767-47827
; Sequence 47827, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47827
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47827

Query Match 38.1%; Score 43; DB 4; Length 190;
Best Local Similarity 42.9%; Pred. No. 53;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTVA---GAMLAAP 21
| | | | | | | | | | | | | | | | | | | |
Db 7 IKRIAETAVAYAKAGAHIVAP 27

RESULT 40
5217891-15
; Patent No. 5217891
; APPLICANT: BRAKE, ANTHONY J.;VAN DEN BERG, JOHAN A.
; TITLE OF INVENTION: DNA CONSTRUCTS CONTAINING A KLUYVEROMYCES
; A FACTOR LEADER SEQUENCE FOR DIRECTING SECRETION OF HETEROLOGOUS
; POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/507,398
; FILING DATE: 09-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 78,551
; FILING DATE: 28-JUL-1987
; SEQ ID NO.15:
; LENGTH: 458
5217891-15

Query Match 38.1%; Score 43; DB 6; Length 458;
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
Matches 10; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTVA---GAMLAAPVAT 24
| | | | | | | | | | | | | | | | | | | |
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Db 1 MKFSTILAASTALISVVMAPVST 24

Search completed: December 1, 2004, 11:51:38
Job time : 39 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2004, 11:50:21 ; Search time 145 Seconds
(without alignments)
61.487 Million cell updates/sec

Title: US-10-673-860-3

Perfect score: 113
Sequence: 1 MKRMKSLAALTAVAGMLAAPVATA 25

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Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 35623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
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20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	113	100.0	25	14	US-10-112-488-2
2	113	100.0	25	16	US-10-673-860-3
3	57	50.4	395	9	US-09-738-626-6644
4	55	48.7	526	16	US-10-437-963-190930
5	51.5	45.6	87	14	US-10-156-761-12894
6	51	45.1	104	9	US-09-738-626-4865
7	51	45.1	107	14	US-10-193-002-84
8	51	45.1	107	14	US-10-084-843-83
9	51	45.1	168	14	US-10-080-170-534
10	51	45.1	168	14	US-10-193-002-95
11	51	45.1	168	14	US-10-084-843-100
12	51	45.1	168	16	US-10-080-170-534
13	51	45.1	168	17	US-10-468-356-534
					Sequence 2, Appl
					Sequence 3, Appl
					Sequence 644, Ap
					Sequence 190930,
					Sequence 12894, A
					Sequence 4865, Ap
					Sequence 84, Appl
					Sequence 83, Appl
					Sequence 534, App
					Sequence 95, Appl
					Sequence 100, App
					Sequence 534, App
					Sequence 534, App

51	45.1	187	14	US-10-193-002-64	Sequence 64, Appl
51	45.1	187	14	US-10-084-843-63	Sequence 63, Appl
50	44.2	56	11	US-09-864-486A-8468	Sequence 8468, Ap
50	44.2	279	9	US-09-738-626-3942	Sequence 3942, Ap
49	43.4	66	17	US-10-425-115-326373	Sequence 326373,
48	42.5	132	15	US-10-389-566-1646	Sequence 1646, Ap
48	42.5	166	17	US-10-425-115-335695	Sequence 335695,
48	42.5	254	16	US-10-437-963-196448	Sequence 196448,
48	42.5	255	15	US-10-425-114-49108	Sequence 49108, A
48	42.5	500	16	US-10-437-963-190010	Sequence 190010,
48	42.5	998	15	US-10-282-122A-50795	Sequence 50795, A
48	42.5	1234	15	US-10-282-122A-66333	Sequence 66333, A
48	42.5	236	15	US-10-424-599-266117	Sequence 266117,
47	41.6	260	15	US-10-282-122A-69738	Sequence 69738, A
47	41.6	409	15	US-10-282-122A-49262	Sequence 49262, A
47	41.6	458	14	US-10-213-181-14	Sequence 14, Appl
47	41.6	458	14	US-10-213-914-14	Sequence 14, Appl
47	41.6	458	14	US-10-213-044-14	Sequence 14, Appl
47	41.6	458	14	US-10-213-182-14	Sequence 14, Appl
47	41.6	458	14	US-10-213-060A-14	Sequence 14, Appl
47	41.6	458	14	US-10-213-052-14	Sequence 14, Appl
47	41.6	489	14	US-10-273-517-4	Sequence 4, Appl
47	41.6	489	15	US-10-311-104-4	Sequence 4, Appl
46.5	41.2	85	17	US-10-425-115-213257	Sequence 213257,
46.5	41.2	196	14	US-10-243-552-496	Sequence 496, App
46	40.7	81	14	US-10-156-761-14005	Sequence 14005, A
46	40.7	114	16	US-10-437-963-191208	Sequence 191208,
46	40.7	167	16	US-10-437-963-203943	Sequence 203943,
46	40.7	231	14	US-10-156-761-11024	Sequence 11024, A
46	40.7	239	14	US-10-156-761-8154	Sequence 8154, App
46	40.7	361	16	US-10-437-963-146049	Sequence 146049,
46	40.7	537	16	US-10-676-358-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-112-488-2
; Sequence 2, Application US/10112488
; Publication No. US20030082746A1
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, Yoshiaki
; APPLICANT: DATE, Masayo
; APPLICANT: UMEZAWA, Yukiko
; APPLICANT: YOKOYAMA, Keiichi
; APPLICANT: MATSUI, Hiroshi
; TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSLUTAMINASE
; FILE REFERENCE: 219286USOCONT
; CURRENT APPLICATION NUMBER: US/10/112,488
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: PCT/JP00/06780
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: JP2000-280098
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: JP11-280098
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 25
; TYPE: PXT
; ORGANISM: Corynebacterium ammoniagenes
US-10-112-488-2

Query Match 100.0%; Score 113; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRMKSLAALTAVAGMLAAPVATA 25

Db 1 MKRMKSLAALTAVAGMLAAPVATA 25

RESULT 2
US-10-673-860-3
; Sequence 3, Application US/10673860
; Publication No. US20040126847A1
; GENERAL INFORMATION:
; APPLICANT: Ajinomoto Co., Inc.
; TITLE OF INVENTION: A method of secreting and producing proteins
; FILE REFERENCE: YJ0182
; CURRENT APPLICATION NUMBER: US/10/673,860
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: JP 2001-98808
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; TYPE: 25
; LENGTH: 25
; ORGANISM: Corynebacterium ammoniagenes
US-10-673-860-3

Query Match 100.0%; Score 113; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRMKSLAALTVAGAMLAAPVATA 25
|||||
Db 1 MKRMKSLAALTVAGAMLAAPVATA 25
|||||

RESULT 3
US-09-738-626-6644
; Sequence 6644, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent In ver. 3.0
; SEQ ID NO 6644
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6644

Query Match 50.4%; Score 57; DB 9; Length 395;
Best Local Similarity 66.7%; Pred. No. 4.6;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 MKRMKSLAALTVAGAMLA 19
|||
Db 13 KRLKPLAAAVAVGVLLA 30
|||

RESULT 4

US-10-437-963-190930
; Sequence 190930, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 190930
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(526)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_87298C.1.pap
US-10-437-963-190930

Query Match 48.7%; Score 55; DB 16; Length 526;
Best Local Similarity 54.2%; Pred. No. 12;
Matches 13; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 KRMKSLAALTVAGAMLAAPVATA 25
|||
Db 6 RRRSRRAAALVLAALLAASATA 29
|||

RESULT 5
US-10-156-761-12894
; Sequence 12894, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12894
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12894

Query Match 45.6%; Score 51.5; DB 14; Length 87;
Best Local Similarity 65.2%; Pred. No. 5.5;
Matches 15; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 4 MKSLAALTVAGAM-LAAPVATA 25
|||
Db 1 MKSLKAAAVVAGSNVLGAVAPA 23
|||

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CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/193,002
  FILING DATE: 10-Jul-2002
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/072,596
  FILING DATE: 05-MAY-1998
  ATTORNEY/AGENT INFORMATION:
    NAME: Maki, David J.
  REGISTRATION NUMBER: 31,392
  REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (206) 622-4900
  TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 84:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 107 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-193-002-84
Query Match      45.1%; Score 51; DB 14; Length 107;
Best Local Similarity 60.0%; Pred. No. 8.2;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 MKRMKSLAAALTVAGAMLA 20
      |||:|||||:|||||:
Db      10 MKVMKSLAAGLTAAAGAA 29

RESULT 8
US-10-084-843-83
  Sequence 83, Application US/10084843
  Publication No. US20030143243A1
  GENERAL INFORMATION:
    APPLICANT: Reed, Steven G.
    Skeiky, Yasir A.W.
    Dillon, Davin C.
    Campos-Neto, Antonio
    Houghton, Raymond
    Vedwick, Thomas S.
    Twardzik, Daniel R.
    Lodes, Michael J.
    Hendrickson, Ronald C.
  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
    AND DIAGNOSIS OF TUBERCULOSIS
  NUMBER OF SEQUENCES: 355
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: SEED and BERRY LLP
    STREET: 6300 Columbia Center, 701 Fifth Avenue
    CITY: Seattle
    STATE: Washington
    COUNTRY: USA
    ZIP: 98104-7092
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/084,843
    FILING DATE: 25-Feb-2002
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/072,967
    FILING DATE: 05-MAY-1998
    ATTORNEY/AGENT INFORMATION:
      NAME: Maki, David J.
    REGISTRATION NUMBER: 31,392
    REFERENCE/DOCKET NUMBER: 210121.411C9
  TELECOMMUNICATION INFORMATION:

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US-09-738-626-4865
  Sequence 4865, Application US/09738626
  Publication No. US20020197605A1
  GENERAL INFORMATION:
    APPLICANT: NAKAGAWA, SATOSHI
    APPLICANT: MIZOGUCHI, HIROSHI
    APPLICANT: ANDO, SEIKO
    APPLICANT: HAYASHI, MIKIRO
    APPLICANT: OCHIAI, KEIKO
    APPLICANT: YOKOI, HARUHIKO
    APPLICANT: TATEISHI, NAKO
    APPLICANT: SENOH, AKIHIRO
    APPLICANT: IKEDA, MASATO
    APPLICANT: OZAKI, AKIO
  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
  FILE REFERENCE: 249-125
  CURRENT APPLICATION NUMBER: US/09/738,626
  CURRENT FILING DATE: 2000-12-18
  PRIOR APPLICATION NUMBER: JP 99/377484
  PRIOR FILING DATE: 1999-12-16
  PRIOR APPLICATION NUMBER: JP 00/159162
  PRIOR FILING DATE: 2000-04-07
  PRIOR APPLICATION NUMBER: JP 00/280988
  PRIOR FILING DATE: 2000-08-03
  NUMBER OF SEQ ID NOS: 7059
  SOFTWARE: PatentIn ver. 3.0
  SEQ ID NO 4865
  LENGTH: 104
  TYPE: PRT
  ORGANISM: Corynebacterium glutamicum
US-09-738-626-4865
Query Match      45.1%; Score 51; DB 9; Length 104;
Best Local Similarity 48.0%; Pred. No. 7.9;
Matches 12; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy      1 MKRMKSLAAALTVAGAMLAAPVATA 25
      |||:|||||:|||||:
Db      2 IKKYLSTIAAVTASAVLFPASAQA 26

RESULT 7
US-10-193-002-84
  Sequence 84, Application US/10193002
  Publication No. US20030135026A1
  GENERAL INFORMATION:
    APPLICANT: Reed, Steven G.
    Skeiky, Yasir A.W.
    Dillon, Davin C.
    Campos-Neto, Antonia
    Houghton, Raymond
    Vedwick, Thomas S.
    Twardzik, Daniel R.
    Lodes, Michael J.
    Hendrickson, Ronald C.
  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
    TUBERCULOSIS
  NUMBER OF SEQUENCES: 350
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: SEED and BERRY LLP
    STREET: 6300 Columbia Center, 701 Fifth Avenue
    CITY: Seattle
    STATE: Washington
    COUNTRY: USA
    ZIP: 98104-7092
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30

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```

; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-10-084-843-83

Query Match 45.1%; Score 51; DB 14; Length 107;
Best Local Similarity 60.0%; Pred. No. 8.2;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTVAGAMLAA 20
Db 10 MKMVKSIAAGLTAAAGAA 29

RESULT 9
US-10-080-170-534
; Sequence 534, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 534
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-534

Query Match 45.1%; Score 51; DB 14; Length 168;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTVAGAMLAA 20
Db 1 MKMVKSIAAGLTAAAGAA 20

RESULT 10
US-10-193-002-95
; Sequence 95, Application US/10193002
; Publication No. US20030135026A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; Skeiky, Yasir A.W.
; Dillon, Davin C.
; Campos-Neto, Antonia
; Houghton, Raymond
; Vedvick, Thomas S.
; Twardzik, Daniel R.
; Lodes, Michael J.
; Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TUBERCULOSIS
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington

```

```

; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/193,002
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,596
; FILING DATE: 05-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-10-193-002-95

Query Match 45.1%; Score 51; DB 14; Length 168;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTVAGAMLAA 20
Db 1 MKMVKSIAAGLTAAAGAA 20

RESULT 11
US-10-084-843-100
; Sequence 100, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; Skeiky, Yasir A.W.
; Dillon, Davin C.
; Campos-Neto, Antonio
; Houghton, Raymond
; Vedvick, Thomas S.
; Twardzik, Daniel R.
; Lodes, Michael J.
; Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/084,843
; FILING DATE: 25-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-084-843-100

Query Match 45.1%; Score 51; DB 14; Length 168;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAALTVAGAMLAA 20
Db 1 MKMKVKSIAAGLTAAAGAA 20

RESULT 12

US-10-080-170-534
Sequence 534, Application US/10080170
Publication No. US20040121322A9
GENERAL INFORMATION:
APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 534
LENGTH: 168
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-10-080-170-534

Query Match 45.1%; Score 51; DB 16; Length 168;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAALTVAGAMLAA 20
Db 1 MKMKVKSIAAGLTAAAGAA 20

RESULT 13

US-10-468-356-534
Sequence 534, Application US/10468356
Publication No. US20040197896A1
GENERAL INFORMATION:
APPLICANT: COLE, STEWART
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 05394.0019
CURRENT APPLICATION NUMBER: US/10/468,356
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: 10/080,170
PRIOR FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/270,123

PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 655
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 534
LENGTH: 168
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-10-468-356-534

Query Match 45.1%; Score 51; DB 17; Length 168;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAALTVAGAMLAA 20
Db 1 MKMKVKSIAAGLTAAAGAA 20

RESULT 14

US-10-193-002-64
Sequence 64, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Wedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-10-193-002-64

Query Match 45.1%; Score 51; DB 14; Length 187;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKMKSLAAALTAVAGAMLAA 20
 Db 20 MKMKSLAAALTAVAGAMLAA 39

RESULT 15
 US-10-843-843-63
 ; Sequence 63, Application US/10084843
 ; Publication No. US20030143243A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; Skeiky, Yasir A.W.
 ; Dillon, Davin C.
 ; Campos-Neto, Antonio
 ; Houghton, Raymond
 ; Vedvick, Thomas S.
 ; Twardzik, Daniel R.
 ; Lodes, Michael J.
 ; Hendrickson, Ronald C.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 ; AND DIAGNOSIS OF TUBERCULOSIS
 ; NUMBER OF SEQUENCES: 355
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/084,843
 ; FILING DATE: 25-Feb-2002
 ; CLASSIFICATION: <unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/072,967
 ; FILING DATE: 05-MAY-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Maki, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.411C9
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 63:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 187 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 63:
 US-10-843-843-63

Query Match 45.1%; Score 51; DB 14; Length 187;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKMKSLAAALTAVAGAMLAA 20
 Db 20 MKMKSLAAALTAVAGAMLAA 39

RESULT 16
 US-09-864-408A-8468
 ; Sequence 8468, Application US/09864408A
 ; Publication No. US20040009474A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leach, Martin D.

; APPLICANT: Shimkets, Richard A.
 ; TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Enco
 ; FILE REFERENCE: 21402-012
 ; CURRENT APPLICATION NUMBER: US/09/864,408A
 ; CURRENT FILING DATE: 2001-05-24
 ; PRIOR APPLICATION NUMBER: 60/206,690
 ; PRIOR FILING DATE: 2000-05-24
 ; NUMBER OF SEQ ID NOS: 9068
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8468
 ; LENGTH: 56
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-864-408A-8468

Query Match 44.2%; Score 50; DB 11; Length 56;
 Best Local Similarity 50.0%; Pred. No. 5.6;
 Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKMKSLAAALTAVAGAMLAA 24
 Db 1 MKMKSLAAALTAVAGAMLAA 24

RESULT 17
 US-09-738-626-3942
 ; Sequence 3942, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAOKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: Patent in ver. 3.0
 ; SEQ ID NO 3942
 ; LENGTH: 279
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-09-738-626-3942

Query Match 44.2%; Score 50; DB 9; Length 279;
 Best Local Similarity 48.0%; Pred. No. 33;
 Matches 12; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MKMKSLAAALTAVAGAMLAA 25
 Db 1 MKMKSLAAALTAVAGAMLAA 25

RESULT 18
 US-10-425-115-326373
 ; Sequence 326373, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 326373
LENGTH: 66
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_60722C.1.pap
US-10-425-115-326373

Query Match 43.4%; Score 49; DB 17; Length 66;
Best Local Similarity 45.8%; Pred. No. 9.5;
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTVAGAMLAAPVAT 24
Db 1 MARTQSVAVFVVPVILLAPAT 24

RESULT 19
US-10-389-566-1646
Sequence 1646, Application US/10389566
Publication No. US20040025202A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52900)D
CURRENT APPLICATION NUMBER: US/10/389,566
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1646
LENGTH: 132
TYPE: PRT
ORGANISM: Thermosynechococcus elongatus
US-10-389-566-1646

Query Match 42.5%; Score 48; DB 15; Length 132;
Best Local Similarity 57.9%; Pred. No. 29;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 7 LAAALTVAGAMLAAPVATA 25
Db 33 VSAAPVGMVAAPVAGA 51

RESULT 20
US-10-425-115-335695
Sequence 335695, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 335695
LENGTH: 166
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_6925C.1.pap
US-10-425-115-335695

Query Match 42.5%; Score 48; DB 17; Length 166;
Best Local Similarity 51.9%; Pred. No. 37;
Matches 14; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

Qy 1 MKRMKS-LAAALTVAGAMLAAPVATA 25
Db 6 LARSKSLHIVALTTPAAKXATPIAGA 32

RESULT 21
US-10-437-963-196448
Sequence 196448, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 196448
LENGTH: 254
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(254)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_92299C.1.pap
US-10-437-963-196448

Query Match 42.5%; Score 48; DB 16; Length 254;
Best Local Similarity 61.1%; Pred. No. 59;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 7 LAAALTVAGAMLAAPVAT 24
Db 227 LAASVLVVGASLAAPPAS 244

RESULT 22
US-10-425-114-49108
Sequence 49108, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114

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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49106
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700048791_FLI.pep
US-10-425-114-49108

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Query Match 42.5%; Score 48; DB 15; Length 255;
Best Local Similarity 51.9%; Pred. No. 60;
Matches 14; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

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QY 1 MKRMKS--LAALTVAGAMLAAPVATA 25
DB 42 LARSKSLHLVAALTPAAKAAATPIAGA 68

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RESULT 23
US-10-437-963-190010
; Sequence 190010, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

```

```

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

```

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; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)/B

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; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14

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; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 190010
; LENGTH: 500
; TYPE: PRT

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; ORGANISM: Oryza sativa
; FEATURE:

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; OTHER INFORMATION: Clone ID: PAT_MRT4530_86464C.1.pep
US-10-437-963-190010

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Query Match 42.5%; Score 48; DB 16; Length 500;
Best Local Similarity 68.8%; Pred. No. 1.3e+02;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY 10 ALTAVAGAMLAAPVATA 25
DB 153 ALTAVAGVIFIAAVATA 168

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RESULT 24
US-10-282-122A-50795
; Sequence 50795, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

```

```

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50795
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-10-282-122A-50795

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Query Match 42.5%; Score 48; DB 15; Length 998;
Best Local Similarity 52.4%; Pred. No. 2.7e+02;
Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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QY 3 RKXSLAALTAVAGAMLAAPVA 23
DB 9 RLHAAALALAGMARLAPAA 29

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RESULT 25
US-10-282-122A-66333
; Sequence 66333, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

```

```

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578

```

```
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66333
; LENGTH: 1234
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66333

Query Match 42.5%; Score 48; DB 15; Length 1234;
Best Local Similarity 59.1%; Pred. No. 3.4e+02;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 MKSLAAALTAVAGMLAAPVATA 25
Db 103 MOSLAYELNVEGARLARQVADA 124

RESULT 26
US-10-424-599-266117
; Sequence 266117, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 266117
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(236)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_82324C.1.pep
US-10-424-599-266117

Query Match 41.6%; Score 47; DB 15; Length 236;
Best Local Similarity 47.8%; Pred. No. 77;
Matches 11; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 2 KRMKSLAAALTAVAGMLAAPVAT 24
Db 10 KKQKXAAQAQAAAAAAAPTAS 32

RESULT 27
US-10-282-122A-69738
; Sequence 69738, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69738
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Pseudomonas syringae
US-10-282-122A-69738

Query Match 41.6%; Score 47; DB 15; Length 260;
Best Local Similarity 50.0%; Pred. No. 86;
Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGMLAAPV 22
Db 1 MRFLGSLLLALSITGAHAAPV 22

RESULT 28
US-10-282-122A-49262
; Sequence 49262, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
```


; SEQ ID NO 14
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-213-044-14
Query Match 41.6%; Score 47; DB 14; Length 458;
Best Local Similarity 59.1%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 4 MKSLAAALTAVAGAMLAAPVATA 25
| : ||||| ||||| |||||
Db 1 MRGLAVLLTVALATLLAPGAGA 22
RESULT 32
US-10-213-182-14
; Sequence 14, Application US/10213182
; Publication No. US20030087380A1
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P3133RIC3
; CURRENT APPLICATION NUMBER: US/10/213,182
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/052,594
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/172,059
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 14
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-213-182-14
Query Match 41.6%; Score 47; DB 14; Length 458;
Best Local Similarity 59.1%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 4 MKSLAAALTAVAGAMLAAPVATA 25
| : ||||| ||||| |||||
Db 1 MRGLAVLLTVALATLLAPGAGA 22
RESULT 33
US-10-213-060A-14
; Sequence 14, Application US/10213060A
; Publication No. US20030100063A1
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P3133RIC4
; CURRENT APPLICATION NUMBER: US/10/213,060A
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 10/052,594
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/172,059
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 14
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-213-060A-14
Query Match 41.6%; Score 47; DB 14; Length 458;
Best Local Similarity 59.1%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 4 MKSLAAALTAVAGAMLAAPVATA 25
| : ||||| ||||| |||||
Db 1 MRGLAVLLTVALATLLAPGAGA 22
RESULT 34
US-10-213-052-14
; Sequence 14, Application US/10213052
; Publication No. US20030153015A1
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P3133RIC5
; CURRENT APPLICATION NUMBER: US/10/213,052
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/052,594
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/177,118
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 14
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-213-052-14
Query Match 41.6%; Score 47; DB 14; Length 458;
Best Local Similarity 59.1%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 4 MKSLAAALTAVAGAMLAAPVATA 25
| : ||||| ||||| |||||
Db 1 MRGLAVLLTVALATLLAPGAGA 22
RESULT 35
US-10-273-517-4
; Sequence 4, Application US/10273517
; Publication No. US20030143588A1
; GENERAL INFORMATION:

; SEQ ID NO 14
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-213-044-14
Query Match 41.6%; Score 47; DB 14; Length 458;
Best Local Similarity 59.1%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 4 MKSLAAALTAVAGAMLAAPVATA 25
| : ||||| ||||| |||||
Db 1 MRGLAVLLTVALATLLAPGAGA 22
RESULT 32
US-10-213-182-14
; Sequence 14, Application US/10213182
; Publication No. US20030087380A1
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P3133RIC3
; CURRENT APPLICATION NUMBER: US/10/213,182
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/052,594
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/172,059
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 14
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-213-182-14
Query Match 41.6%; Score 47; DB 14; Length 458;
Best Local Similarity 59.1%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 4 MKSLAAALTAVAGAMLAAPVATA 25
| : ||||| ||||| |||||
Db 1 MRGLAVLLTVALATLLAPGAGA 22
RESULT 33
US-10-213-060A-14
; Sequence 14, Application US/10213060A
; Publication No. US20030100063A1
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P3133RIC3
; CURRENT APPLICATION NUMBER: US/10/213,182
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/052,594
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/172,059
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 14
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-213-182-14
Query Match 41.6%; Score 47; DB 14; Length 458;
Best Local Similarity 59.1%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 4 MKSLAAALTAVAGAMLAAPVATA 25
| : ||||| ||||| |||||
Db 1 MRGLAVLLTVALATLLAPGAGA 22
RESULT 34
US-10-213-052-14
; Sequence 14, Application US/10213052
; Publication No. US20030153015A1
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P3133RIC5
; CURRENT APPLICATION NUMBER: US/10/213,052
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/052,594
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/177,118
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 14
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-213-052-14
Query Match 41.6%; Score 47; DB 14; Length 458;
Best Local Similarity 59.1%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 4 MKSLAAALTAVAGAMLAAPVATA 25
| : ||||| ||||| |||||
Db 1 MRGLAVLLTVALATLLAPGAGA 22
RESULT 35
US-10-273-517-4
; Sequence 4, Application US/10273517
; Publication No. US20030143588A1
; GENERAL INFORMATION:

;; PRIOR APPLICATION NUMBER: PCT/US01/03800
;; PRIOR FILING DATE: 2001-02-05
;; PRIOR APPLICATION NUMBER: US 09/496,914
;; PRIOR FILING DATE: 2000-02-03
;; PRIOR APPLICATION NUMBER: US 09/560,875
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: PCT/US01/04927
;; PRIOR FILING DATE: 2001-02-26
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 998
;; SOFTWARE: pt_FL_genes Version 5.0
;; SEQ ID NO 496
;; LENGTH: 196
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-243-552-496

Query Match 41.2%; Score 46.5; DB 14; Length 196;
Best Local Similarity 59.1%; Pred. No. 74;
Matches 13; Conservative 2; Mismatches 4; Indels 3; Gaps 1;
QY 7 LAAALTVAGAML---AAPVATA 25
| | | | | : | | | | : | | | |
Db 21 LAAALLAAFLALATALPIATA 42

RESULT 39
US-10-156-761-14005
;; Sequence 14005, Application US/10156761
;; Publication No. US20030119018A1
;; GENERAL INFORMATION:
;; APPLICANT: OMURA, SATOSHI
;; APPLICANT: IKEDA, HARUO
;; APPLICANT: ISHIKAWA, JUN
;; APPLICANT: HORIKAWA, HIROSHI
;; APPLICANT: SHIBA, TADAYOSHI
;; APPLICANT: SAKAKI, YOSHIYUKI
;; APPLICANT: HATTORI, MASAHIRA
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;; FILE REFERENCE: 249-262
;; CURRENT APPLICATION NUMBER: US/10/156,761
;; PRIOR FILING DATE: 2002-05-29
;; PRIOR APPLICATION NUMBER: JP 2001-204089
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: JP 2001-272697
;; PRIOR FILING DATE: 2001-08-02
;; NUMBER OF SEQ ID NOS: 15109
;; SEQ ID NO 14005
;; LENGTH: 81
;; TYPE: PRT
;; ORGANISM: Streptomyces avermitilis
US-10-156-761-14005

Query Match 40.7%; Score 46; DB 14; Length 81;
Best Local Similarity 40.0%; Pred. No. 33;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
QY 1 MKRMKSLAAALTVAGAMLAAPVATA 25
: | | | | : | | | | : | | | |
Db 1 VKNLKKVAAVTMTVAGGLVAAGAWA 25

RESULT 40
US-10-437-963-191208
;; Sequence 191208, Application US/10437963
;; Publication No. US20040123343A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa, Thomas J.
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Cao, Yongwei
;; APPLICANT: Wu, Wei
;; APPLICANT: Boukharov, Andrey A.

;; APPLICANT: Barbazuk, Brad
;; APPLICANT: Li, Ping
;; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;; FILE REFERENCE: 38-21(53221)B
;; CURRENT APPLICATION NUMBER: US/10/437,963
;; CURRENT FILING DATE: 2003-05-14
;; NUMBER OF SEQ ID NOS: 204966
;; SEQ ID NO 191208
;; LENGTH: 114
;; TYPE: PRT
;; ORGANISM: Oryza sativa
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT4530_87548C.1.pep
US-10-437-963-191208

Query Match 40.7%; Score 46; DB 16; Length 114;
Best Local Similarity 47.6%; Pred. No. 48;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 2 KRMKSLAAALTVAGAMLAAPV 22
: | | | | : | | | | : | | | |
Db 18 RQLQLLVAALSTAGAVAAAV 38

Search completed: December 1, 2004, 12:02:32
Job time : 146 secs

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Db 1 MRMRKSIRAAUTAAATVAA 20
 :|||:|||||:|

RESULT 3

JC1287
 ribonuclease Sa (EC 3.1.1.27.-) precursor - Streptomyces aureofaciens (strain CCM3239)
 N:Alternate names: guanyloribonuclease; ribonuclease Sa3
 C:Species: Streptomyces aureofaciens
 C>Date: 30-Sep-1993 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
 C:Accession: JC1287
 R:Homerova, D.; Hollaenderova, Z.; Kormanec, J.; Sevcik, J.
 Gene 119, 147-148, 1992
 A:Title: Cloning and sequencing of the gene encoding a ribonuclease from Streptomyces aureofaciens
 A:Reference number: JC1287; MUID:93012968; PMID:11398084
 A:Accession: JC1287
 A:Molecule type: DNA
 A:Residues: 1-141 <HOW>
 A:Cross-references: UNIPROT:P30289; GB:M82920
 A:Experimental source: strain CCM3239
 C:Superfamily: ribonuclease Sa
 C:Keywords: extracellular protein; hydrolase
 F:i-28/Domain: (or 1-34) signal sequence #status predicted <SIG>
 F:29-141/Product: (or 35-141) ribonuclease #status predicted <MAT>

Query Match 46.0%; Score 52; DB 1; Length 141;
 Best Local Similarity 47.8%; Pred. No. 3.5;
 Matches 11; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RMKSLAAALTIVAGAMLAAPVATA 25
 :|||:|||||:|
 Db 6 RLVALAGAAVAATLIAGPVAAA 28
 :|||:|||||:|

RESULT 4

G70587
 hypothetical protein Rv2376c - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: G70587
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: G70587
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-168 <COL>
 A:Cross-references: UNIPROT:O05822; GB:Z95208; GB:AL123456; NID:G3261747; PIDN:CAB08476.
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: Rv2376c

Query Match 45.1%; Score 51; DB 2; Length 168;
 Best Local Similarity 60.0%; Pred. No. 5.6;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRMRKSLAAALTIVAGAMLA 20
 :|||:|||||:|
 Db 1 MRMRKSLAAALTIVAGAMLA 20
 :|||:|||||:|

RESULT 5

H71723
 ribosomal protein L7/L12 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
 C:Accession: H71723
 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alsmark, T.
 Nature 396, 133-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A:Reference number: A71630; MUID:99039499; PMID:9823893
 A:Accession: H71723
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-125 <AND>
 A:Cross-references: UNIPROT:Q9221; GB:AJ235270; GB:AJ235269; NID:G3860572; PIDN:CAA1460
 A:Experimental source: strain Madrid E
 C:Genetics:
 A:Gene: rplL; RPl39
 C:Superfamily: Escherichia coli ribosomal protein L12

Query Match 44.2%; Score 50; DB 2; Length 125;
 Best Local Similarity 60.0%; Pred. No. 6;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 6 SLAAALTIVAGAMLAAPVATA 25
 :|||:|||||:|
 Db 33 SAAAPITVASRGVAPLAEA 52
 :|||:|||||:|

RESULT 6

T36861
 probable small secreted protein - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T36861
 R:Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, June 1999
 A:Reference number: Z21616
 A:Accession: T36861
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-82 <SEE>
 A:Cross-references: UNIPROT:Q9X9Z2; EMBL:AL079332; PIDN:CAB45292.1; GSPDB:GN00070; SCORED
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEBS-SC15.08c

Query Match 43.4%; Score 49; DB 2; Length 82;
 Best Local Similarity 44.0%; Pred. No. 5.8;
 Matches 11; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTIVAGAMLAAPVATA 25
 :|||:|||||:|
 Db 1 MKNLKAAAVTWAGGLIAGAGWA 25
 :|||:|||||:|

RESULT 7

F90884
 probable transport system permease protein Ecs2046 [imported] - Escherichia coli (strain C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C:Accession: F90884
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Sasawara, T.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: F90884
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-313 <HAY>
 A:Cross-references: UNIPROT:Q8X9W3; GB:BA000007; PIDN:BA35469.1; PID:G13361512; GSPDB:G
 A:Experimental source: strain O157:H7, substrain XMD 0509952
 C:Genetics:
 A:Gene: Ecs2046
 C:Superfamily: spermidine/putrescine transport system permease protein potH

Query Match 43.4%; Score 49; DB 2; Length 313;
 Best Local Similarity 47.6%; Pred. No. 18;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 RMKSLAAALTVAGAMLAAPVA 23
 | : : | : | : | : | : |
Db 89 RLTMAVAVTIAAAILAFPM 109

RESULT 8

A857334
probable transport system permease protein Z2277 [imported] - *Escherichia coli* (strain C
C; Species: *Escherichia coli*
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C; Accession: A857334
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A; Reference number: A85480; MWID:21074935; PMID:11206551
A; Accession: A85734
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-313 <STOP>
A; Cross-references: UNIPROT:Q9X9W3; GB:AE0051174; NID:gl2515260; PIDN:AA656333.1; GSPDB:G
A; Experimental source: strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: Z2277
C; Superfamily: spermidine/putrescine transport system permease protein both

```

Query Match      43.4%; Score
Best Local Similarity 47.6%; Pred.
Matches 10; Conservative 6; Mismatches 1
QY      3 RMKSLAALTVAGAMLAAPVA 23
      | : : : : : : : : : :
Db      89 RTITMAVATVATASALIAFPMA 109

```

RESULT 9

E64896
probable membrane protein b1442 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C/Accession: E64896
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: E64896
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-313 <BLAST>
A:CROSS-references: UNIPROT:P77156; GB:AE000241; GB:U00096; NID:gl787706; PIDN:AC74524.
A:Experimental source: Strain K-12, substrain MG1655
C:Superfamily: Spermidine/putrescine transport system permease protein pOTH
C:Keywords: inner membrane; transmembrane protein
F:27-43/Domain: transmembrane #status predicted <TM1>
F:90-106/Domain: transmembrane #status predicted <TM2>
F:122-138/Domain: transmembrane #status predicted <TM3>
F:188-204/Domain: transmembrane #status predicted <TM4>
F:232-248/Domain: transmembrane #status predicted <TM5>
F:288-304/Domain: transmembrane #status predicted <TM6>

Query Match 43.4%; Score 49; DB 2; Length 313;
Best Local Similarity 47.6%; Pred. No. 18;
Matches 10: Conservative 6; Mismatches 5: Indels

QY 3 RMKSLAAALT VAGAMIAAPVA 23
| : | : | : | : | : | :
Db 89 RTLTMAVAVT IASAILAFPPA 109

RESULT 10

RESOL 10
JCI439
glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) VI - barley

N:Alternate names: endo-1,3-beta-glucanase
C:Species: Hordeum vulgare (barley)
C:Date: 30-Sep-1993 #sequence_revision 30-
C:Accession: Jc1439
E:Xu, P.; Wang, J.; Fincher, G.B.

A;Title: Evolution and differential expression of the (

A;Accession: JCL1439
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-317 <XUP>
A;Cross-references: GB:M06941
C;Superfamily: beta-1,3-glucanase
C;Keywords: glycosidase; hydrolase; polysaccharide

Query Match 43.4%; Score 49; DB 2; Length 317;
Best Local Similarity 59.1%; Pred. No. 19;
Matches 13; Conservative 2; Mismatches 5; Indels

Qy 4 MKSLAAALTVAGAMLAPVATA 25
|||: ||| ||| : |||
Db 108 MNLEAALQAAG--LSVPVTTA 127

RESULT 11

hypothetical protein PQ0895 - Pyrococcus horikoshii
C_Species: Pyrococcus horikoshii
C_Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C_Accession: G71078
R_Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto,
M.; Chikuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushid
DNA_Res. 5, 55-76, 1998

A; title: complete sequence and gene-organization of the
A-reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: G71078
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-106 <RAW>
A;Cross-references: UNIPROT:O58639; GB:AP000004; NID:G236131; PIDN:BA29989.1; PID:G32
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0895

Query Match 42.5%; Score 48; DB 2; Length 106;
Best Local Similarity 31.8%; Pred. No. 9.9;
Matches 7; Conservative 11; Mismatches 4; Indels

Qy 1 MKRMKSLAAALTIVAGAMLAAPV 22
:::|: : :|: :|
Db 26 LERLRLTSKIGTAGSIMSIPV 47

RESULT 12

conserved hypothetical protein [imported] - *Sinorhizobium meliloti* (strain 1021) magapla
 C:Species: *Sinorhizobium meliloti*
 C:date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C:Accession: F95868
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhwieser, J.; Chain, P.; Vorkholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:title: The complete sequence of the 1,663-kb pSymB pSymB magaplasmid from the N2-fixing endo
 A:reference number: A95847: MUID:2119f56508: PMD:111451431

A;Accession: F95868
A;Status: preliminary
A:Molecule type: DNA

A:Molecule type: DNA
A:Residues: 1-136 <KUR>

A; Cross-references: UNII

A;Experimental source:

R;Galibert, F.; Finan,

pela, D.; Chain, P.; Cov

[REDACTED]

L.; Hyman, R.W.; Jones, T.
Science 293, 669-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
habault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A36039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMB20222
A:Genome: plasmid

Query Match 42.5%; Score 48; DB 2; Length 136;
Best Local Similarity 52.0%; Pred. No. 12;
Matches 13; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MKRMKSLAALTVAGAMLAAPVATA 25
|||:|||||:|
Db 4 MKTSRILAAALLVVGSLAQAA 28
|||:|||||:|

RESULT 13

A35259
Type 1 fibrillar protein precursor - Actinomyces viscosus
C:Species: Actinomyces viscosus
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 09-Jul-2004
C:Accession: A35259
R:Yeung, M.K.; Cisar, J.O.
J. Bacteriol. 172, 2462-2468, 1990

A:Title: Sequence homology between the subunits of two immunologically and functionally
A:Reference number: A35259; MUID:90236904; PMID:1970561
A:Accession: A35259
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-533 <NEU>
A:Cross-references: UNIPROT:P18477; GB:M32067; NID:G141849; PIDN:AAA62572.1; PID:G141850
C:Keywords: transmembrane protein

Query Match 42.5%; Score 48; DB 2; Length 533;
Best Local Similarity 45.8%; Pred. No. 40;
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 2 KRMKSLAALTVAGAMLAAPVATA 25
|||:|||||:|
Db 7 RRGGLAAMTLAAGALVAPTGA 30
|||:|||||:|

RESULT 14

A48296
Glyoxal oxidase (EC 1.2.3.-) precursor - basidiomycete (Phanerochaete chrysosporium)
C:Species: Phanerochaete chrysosporium
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A48296
R:Kersten, P.J.; Cullen, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 7411-7413, 1993

A:Title: Cloning and characterization of a cDNA encoding glyoxal oxidase, a H-2O-2-produ
A:Reference number: A48296; MUID:93348282; PMID:8346264
A:Accession: A48296
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-559 <KER>
A:Cross-references: UNIPROT:Q01772; GB:L118991
C:Superfamily: Arabidopsis thaliana hypothetical protein F5K20.250
C:Keywords: extracellular protein; glycoprotein; oxidoreductase
F1/2/Domain: signal sequence #status predicted <SIG>

Query Match 42.5%; Score 48; DB 2; Length 559;
Best Local Similarity 52.4%; Pred. No. 42;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 4 MKSLAALTVAGAMLAAPVAT 24
|||:|||||:|
Db 1 MSLSLAVVSLAATLAAPAA 21
|||:|||||:|

RESULT 15

I40329
brkA ptotein - Bordetella pertussis
C:Species: Bordetella pertussis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40329
R:Fernandez, R.C.; Weiss, A.A.
Infect. Immun. 62, 4727-4738, 1994

A:Title: Cloning and sequencing of a Bordetella pertussis serum resistance locus.
A:Reference number: I40329; MUID:95012880; PMID:7927748
A:Accession: I40329
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1010 <RES>

A:Cross-references: UNIPROT:Q45340; EMBL:U12276; NID:G562025; PIDN:AAA51646.1; PID:G5620
C:Genetics:
A:Gene: brkA

Query Match 42.5%; Score 48; DB 2; Length 1010;
Best Local Similarity 52.4%; Pred. No. 69;
Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 3 RMKSLAALTVAGAMLAAPVA 23
|||:|||||:|
Db 21 RLHLLAALALAGMARLAPAA 41
|||:|||||:|

RESULT 16

E83415
methionine synthase PA1843 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: E83415
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 958-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: E83415
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1234 <STO>

A:Cross-references: UNIPROT:Q9I2Q2; GB:AE004610; GB:AE004091; NID:G9947825; PIDN:AAG05233
A:Experimental source: strain PA01
C:Genetics:
A:Gene: meth; PA1843
C:Superfamily: cobalamin-dependent methionine synthase; cobalamin-binding homology

Query Match 42.5%; Score 48; DB 2; Length 1234;
Best Local Similarity 59.1%; Pred. No. 82;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 4 MKSLAALTVAGAMLAAPVATA 25
|||:|||||:|
Db 103 MQSLAVELNVEGARLARQVADA 124
|||:|||||:|

RESULT 17

E90629
hypothetical protein ECs0005 [imported] - Escherichia coli (strain O157:H7, substrain RI
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: E90629
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E90629
A:Status: preliminary
A:Molecule type: DNA

RESULT 20

C87381

sensor histidine kinase DivJ [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: C57381

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonits, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of *Caulobacter crescentus*.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: C87381

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-597 <STO>

A:Cross-references: UNIPROT:Q03228; GB:AE005673; NID:gi34223263; PIDN:AAK23047.1; GSPDB:G

C:Genetics:

A:Gene: CC1063

Query Match 42.0%; Score 47.5; DB 2; Length 597;

Best Local Similarity 64.0%; Pred. No. 52;

Matches 16; Conservative 0; Mismatches 4; Indels 5; Gaps 2;

Qy 6 SLAAALT-VAGAMLA---APVATA 25
||||| ||||| ||||| |||||

Db 101 SLAAVLTVGGGMAAAWCLAPVAAA 125

RESULT 21

AG0016

probable exported protein YP00130 [imported] - *Yersinia pestis* (strain CO92)

C:Species: *Yersinia pestis*

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C:Accession: AG0016

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, N.; 413, 523-527, 2001

A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AG0016

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-597 <STO>

```

C:Genetics:
A:Gene: YPO0130

Query Match          41.6%; Score 47; DB 2; Length 89;
Best Local Similarity 43.5%; Pred. No. 12;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY      1 MKRMKSLAAALTIVAGAMLAPVA 23
      |||::|||::|||
DB      1 MKLLKNMAVALVISGLSFAAIA 23

RESULT 22
H87431
hypothetical protein CCL1472 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: H87431
B:Rienman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87431

```


A;Residues: 1-548 <WHI>
A;Cross-references: UNIPROT:Q9RTK8; GB:AE0002017; GB:AE000513; NID:G6459527; PIDN:AAF1131
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1752
A;Map position: 1

Query Match 41.6%; Score 47; DB 2; Length 548;
Best Local Similarity 52.2%; Pred. No. 56;
Matches 12; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 3 RMKSLAALTVAGMLAAPVATA 25
DB 171 RMLLAGAAGIGVILHAPLAAA 193

RESULT 28
T35189
probable ATP-dependent DNA helicase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35189
R;Seeger, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1998

A;Reference number: Z21571
A;Accession: T35189
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-719 <SEE>
A;Cross-references: UNIPROT:O69992; EMBL:AL022374; PIDN:CAA18513.1; GSPDB:GN00070; SCOE0
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOE0B:SC5B8.05

Query Match 41.6%; Score 47; DB 2; Length 719;
Best Local Similarity 43.5%; Pred. No. 71;
Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 KRKSLAALTVAGMLAAPVAT 24
DB 656 QRLRLAESFTVPGLAALAAAT 678

RESULT 29
A98151
dipeptide transporter protein dppA (truncated) [imported] - Agrobacterium tumefaciens (S
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: A98151
R;Goodner, B.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
A.; Liu, F.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A98151
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-502 <KUR>
A;Cross-references: UNIPROT:Q8U6T7; GB:AE007870; PIDN:AAK88731.1; PID:G15158470; GSPDB:G
C;Genetics:
A;Gene: AGR_L325
A;Map position: linear chromosome

Query Match 41.2%; Score 46.5; DB 2; Length 502;
Best Local Similarity 44.0%; Pred. No. 61;
Matches 11; Conservative 8; Mismatches 5; Indels 1; Gaps 1;
QY 1 MKRMKSLAALTVAGMLAAPVATA 25
DB 1 MKKIQTLTAAL-LASAVLAPALSS 24

RESULT 30
hypothetical protein dppA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AC3137
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC3137
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-502 <KUR>
A;Cross-references: UNIPROT:Q8U6T7; GB:AE008689; PIDN:AAL45513.1; PID:G17743223; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: dppA
A;Map position: linear chromosome

Query Match 40.7%; Score 46; DB 2; Length 124;
Best Local Similarity 41.7%; Pred. No. 22;
Matches 10; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 2 KRKSLAALTVAGMLAAPVATA 25
DB 5 RTIRPLAVAVLLAGGLAAGTAAA 28

RESULT 32
S14023
hypothetical protein 29 - Chlamydomonas reinhardtii transposon
C;Species: Chlamydomonas reinhardtii
C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S14023
R;Day, A.; Roach, J.D.
Nucleic Acids Res. 19, 1259-1266, 1991
A;Title: A transposon with an unusual ITR arrangement from Chlamydomonas reinhardtii con
A;Reference number: S14018; MUID:91232306; PMID:1851555
A;Accession: S14023
A;Status: preliminary

AC3137
hypothetical protein dppA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AC3137
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC3137
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-502 <KUR>
A;Cross-references: UNIPROT:Q8U6T7; GB:AE008689; PIDN:AAL45513.1; PID:G17743223; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: dppA
A;Map position: linear chromosome

Query Match 41.2%; Score 46.5; DB 2; Length 502;
Best Local Similarity 44.0%; Pred. No. 61;
Matches 11; Conservative 8; Mismatches 5; Indels 1; Gaps 1;
QY 1 MKRMKSLAALTVAGMLAAPVATA 25
DB 1 MKKIQTLTAAL-LASAVLAPALSS 24

RESULT 31
H87616
cytochrome c family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: H87616
R;Niernan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87616
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-124 <STO>
A;Cross-references: UNIPROT:Q9A473; GB:AE005673; NID:G13424600; PIDN:AAK24932.1; GSPDB:G
C;Genetics:
A;Gene: CC2970

Query Match 40.7%; Score 46; DB 2; Length 124;
Best Local Similarity 41.7%; Pred. No. 22;
Matches 10; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 2 KRKSLAALTVAGMLAAPVATA 25
DB 5 RTIRPLAVAVLLAGGLAAGTAAA 28

RESULT 32
S14023
hypothetical protein 29 - Chlamydomonas reinhardtii transposon
C;Species: Chlamydomonas reinhardtii
C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S14023
R;Day, A.; Roach, J.D.
Nucleic Acids Res. 19, 1259-1266, 1991
A;Title: A transposon with an unusual ITR arrangement from Chlamydomonas reinhardtii con
A;Reference number: S14018; MUID:91232306; PMID:1851555
A;Accession: S14023
A;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-175 <DAY>

A:Cross-references: UNIPROT:Q99203; EMBL:X56231; NID:g18229; PIDN:CAA39685.1; PID:g13607

C:Genetics:

A:Mobile element: transposon

Query Match 40.7%; Score 46; DB 2; Length 175;
Best Local Similarity 47.8%; Pred. No. 29;
Matches 11; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 3 RWKSLAALTVAGAMLAAPVATA 25

DB 102 RVRSLAGVAVSSLTLDPSATA 124

RESULT 33

T34931

hypothetical protein SC3F9.09 SC3F9.09 - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C:Accession: T34931

R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1998

A:Reference number: Z21562

A:Accession: T34931

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-363 <SEE>

A:Cross-references: UNIPROT:O69949; EMBL:AL023862; PIDN:CAA19632.1; GSPDB:GN00070; SC0E

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SC0E8B-SC3F9.09

Query Match 40.7%; Score 46; DB 2; Length 363;
Best Local Similarity 61.1%; Pred. No. 55;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 8 AAALTAVAGAMLAAPVATA 25

DB 132 AAALTAVAGALTGAGLALA 149

RESULT 34

A26955

alkaline serine proteinase (EC 3.4.21.-) precursor - Yeast (Yarrowia lipolytica)

N:Alternate names: alkaline extracellular proteinase

C:Species: Yarrowia lipolytica, Candida lipolytica

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A26955; A31563

R:Davidow, L.S.; O'Donnell, M.M.; Kaczmarek, F.S.; Pereira, D.A.; DeZeeuw, J.R.; Franke,

J. Bacteriol. 169, 4621-4629, 1987

A:Title: Cloning and sequencing of the alkaline extracellular protease gene of Yarrowia

A:Reference number: A26955; MUID:88007405; PMID:2443483

A:Accession: A26955

A:Molecule type: DNA

A:Residues: 1-454 <DAY>

A:Cross-references: UNIPROT:P09230; GB:M17741; NID:g173242; PIDN:AAA35242.1; PID:g173244

R:Natoba, S.; Fukayama, J.; Wing, R.A.; Ogrzydzak, D.M.

Mol. Cell. Biol. 8, 4904-4916, 1988

A:Title: Intracellular precursors and secretion of alkaline extracellular protease of Ya

A:Reference number: A31563; MUID:89096864; PMID:3211132

A:Accession: A31563

A:Molecule type: DNA

A:Residues: 1-200 <WAT>

A:Superfamily: subtilisin; subtilisin homology

C:Keywords: extracellular protein; hydrolase; serine proteinase

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-157/Domain: propeptide #status predicted <PRO>

F:158-454/Product: serine proteinase #status predicted <MA2>

F:191-411/Domain: subtilisin homology <SBT>

F:200-231.397/Active site: Asp, His, Ser #status predicted

Query Match 40.7%; Score 46; DB 1; Length 454;

Best Local Similarity 58.8%; Pred. No. 66;

Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 LAALTVAGAMLAAPVA 23

DB 3 LATAFTILTAAPLA 19

RESULT 35

A95301

hypothetical protein Sma0599 [imported] - Sinorhizobium meliloti (strain 1021) megaplasm

C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: A95301

R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A:Reference number: A95262; MUID:21396509; PMID:11481432

A:Accession: A95301

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-488 <KUR>

A:Cross-references: UNIPROT:Q922Y5; GB:AE006469; PIDN:AAK64971.1; PID:g14523396; GSPDB:G

A:Experimental source: strain 1021, megaplasmid pSymA

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, A.; Ampe, F.; Barloy-Hubler,

Pala, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: Sma0599

A:Genome: plasmid

Query Match 40.7%; Score 46; DB 2; Length 488;

Best Local Similarity 68.8%; Pred. No. 70;

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 AAALTAVAGAMLAAPVA 23

DB 425 AAAGSAGLILAPVA 440

RESULT 36

G75282

probable glutathione-regulated potassium-efflux system protein KefB - Deinococcus radiod

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: G75282

R:White, O.; Bisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Vanathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: G75282

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-575 <WHI>

A:Cross-references: UNIPROT:Q9RRW8; GB:AE002067; NID:g6460176; PIDN:AAF1191.

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2367

A:Map position: 1

C:Superfamily: glutathione-regulated potassium efflux system protein kefC

Query Match 40.7%; Score 46; DB 2; Length 575;

Best Local Similarity 54.5%; Pred. No. 81;

Matches 12; Conservative 5; Mismatches 3; Indels 2; Gaps 1;

A;Reference number: S45608; MUID:94291666; PMID:8020505
 A;Accession: S45608
 A;Molecule type: protein
 A;Residues: 1-71 <BRU>
 A;Cross-references: UNIPROT:P77799
 A;Experimental source: DSM 149
 A;Accession: S66177
 A;Molecule type: protein
 A;Residues: 1-71 <BR2>
 A;Experimental source: DSM 151
 C;Superfamily: light-harvesting protein alpha chain
 C;Keywords: antenna complex; bacteriochlorophyll; light-harvesting polypeptide; membrane

Query Match 39.8%; Score 45; DB 2; Length 71;
 Best Local Similarity 57.1%; Pred. No. 18;
 Matches 12; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 5 KSLAALTVAGMLAAPVATA 25
 Db 50 KAAARAAAVAPVAPVAPQAPA 70

RESULT 40
 A26986
 hypothetical protein 402 - Streptomyces glaucescens
 C;Species: Streptomyces glaucescens
 C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
 R;Huber, M.; Huettner, R.; Lerch, K.
 Nucleic Acids Res. 15, 8106, 1987
 A;Title: The promoter of the Streptomyces glaucescens mel operon.
 A;Reference number: A26986; MUID:88040431; PMID:3118334
 A;Accession: A26986
 A;Molecule type: DNA
 A;Residues: 1-134 <HUB>
 A;Cross-references: UNIPROT:P55047; GB:Y00457; NID:946917; PIDN:CAA68512.1; PID:946918

Query Match 39.8%; Score 45; DB 2; Length 134;
 Best Local Similarity 41.4%; Pred. No. 32;
 Matches 12; Conservative 5; Mismatches 8; Indels 4; Gaps 1;
 QY 1 MKRMKSLAALTVAGA----MLAAPVATA 25
 Db 4 LSRRLGMAAALAAAGTQAVAPAAATA 32

Search completed: December 1, 2004, 11:50:55
 Job time : 40 secs

QY 4 MKSLAALTVAGMLAAPVATA 25
 Db 334 LKALAAALSV--RLIGFPLATA 353

RESULT 37
 C81729
 Mtr/TnaB/TyO permealase family protein TC0204 [imported] - Chlamydia muridarum (strain N1
 C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: C81729
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwinn, M.; Nelson, M.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 A;Accession: C81729
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-398 <TET>
 A;Cross-references: UNIPROT:Q9PLA3; GB:AE002287; GB:AE002160; NID:G7190237; PIDN:AAF3907
 A;Experimental source: strain Nigg (MoPn)
 C;Genetics:
 A;Gene: TC0204
 C;Superfamily: tyrosine-specific transport protein

Query Match 40.3%; Score 45.5; DB 2; Length 398;
 Best Local Similarity 46.2%; Pred. No. 69;
 Matches 12; Conservative 3; Mismatches 6; Indels 5; Gaps 1;
 QY 5 KSLAALTVAG-----MLAAPVATA 25
 Db 4 KMLGGALIVAGTTIGAGVLAAPVAT 29

RESULT 38
 A28631
 amylase precursor, extracellular - Aeromonas hydrophila
 C;Species: Aeromonas hydrophila
 C;Date: 09-Sep-1988 #sequence_revision 09-Sep-1988 #text_change 16-Aug-2004
 C;Accession: A28631
 R;Gobius, K.S.; Pemberton, J.M.
 J. Bacteriol. 170, 1325-1332, 1988
 A;Title: Molecular cloning, characterization, and nucleotide sequence of an extracellular
 A;Reference number: A28631; MUID:88139196; PMID:2449422
 A;Accession: A28631
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-464 <GOB>
 A;Cross-references: UNIPROT:P22630; GB:N20401; NID:G141869; PIDN:AAA21936.1; PID:G141870
 C;Superfamily: Alpha-amylase; alpha-amylase core homology

Query Match 40.3%; Score 45.5; DB 2; Length 464;
 Best Local Similarity 54.5%; Pred. No. 79;
 Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
 QY 4 MKSLAALTVAGMLAAPVATA 25
 Db 1 MKNTAGILATAG-MLIAPLAHA 21

RESULT 39
 S45608
 light-harvesting protein II B-800/850 alpha chain - Rhodocyclus gelatinosus
 N;Alternate names: peripheral antenna complex B800-850 alpha chain
 C;Species: Rhodocyclus gelatinosus
 C;Date: 10-Dec-1994 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C;Accession: S45608; S66177
 R;Brunsholz, R.A.; Suter, F.; Zuber, H.
 Eur. J. Biochem. 222, 667-675, 1994
 A;Title: Structural and spectral characterisation of the antenna complexes of Rhodocyclu

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OM protein - protein search, using sw model

Run on: December 1, 2004, 11:32:44 ; Search time 153 Seconds

(without alignments)
58.616 Million cell updates/sec

Title: US-10-673-860-3

Perfect score: 113

Sequence: 1 MKRMKSLAAALTVAGAMLAAPVATA 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	100.0	25	AAB81158	Aab81158 SlpA pept
2	113	100.0	25	ABU07388	ABU07388 Coryneform
3	113	100.0	25	ADC64923	ADC64923 Corynebac
4	113	100.0	358	Aaw56155	Aaw56155 Aa cell s
5	57	50.4	395	AAG92890	AAG92890 C glutami
6	51	45.1	104	AAG91111	AAG91111 C glutami
7	51	45.1	107	AAW32371	AAW32371 Mycobacte
8	51	45.1	107	AAW32439	AAW32439 Mycobacte
9	51	45.1	107	AAW64311	AAW64311 Mycobacte
10	51	45.1	107	AAW81674	AAW81674 M. tuberc
11	51	45.1	107	AAW38976	AAW38976 M. tuberc
12	51	45.1	107	AAW39113	AAW39113 M. tuberc
13	51	45.1	168	AAW32393	AAW32393 Mycobacte
14	51	45.1	168	AAW32465	AAW32465 Mycobacte
15	51	45.1	168	AAW64332	AAW64332 Mycobacte
16	51	45.1	168	AAW81699	AAW81699 M. tuberc
17	51	45.1	168	AAW38986	AAW38986 M. tuberc
18	51	45.1	168	AAW39129	AAW39129 M. tuberc
19	51	45.1	168	AAW32454	AAW32454 Mycobacte
20	51	45.1	168	ABU05883	ABU05883 M. tuberc
21	51	45.1	166	AAW32351	AAW32351 Mycobacte
22	51	45.1	186	AAW32419	AAW32419 Mycobacte
23	51	45.1	186	AAW81654	AAW81654 M. tuberc
24	51	45.1	187	AAW64291	AAW64291 Mycobacte
25	51	45.1	187	AAW38956	AAW38956 M. tuberc

26 51 45.1 187 2 AAY39093
27 50 44.2 56 5 ABP35261
28 50 44.2 279 4 AAG90188
29 49 43.4 248 4 AAM20157
30 49 43.4 378 4 AAU54144
31 49 43.4 378 6 ABM50663
32 49 43.4 895 4 ABG29771
33 48 42.5 132 8 ADJ49642
34 48 42.5 405 8 ADJ4916
35 48 42.5 998 6 ABU22871
36 48 42.5 1234 6 ABU38409
37 48 42.5 1234 7 ADI39094
38 47 41.6 260 6 ABU41814
39 47 41.6 409 6 ABU21338
40 47 41.6 458 4 ABA7297
41 47 41.6 458 6 ADA26940
42 47 41.6 458 7 ADE86207
43 47 41.6 458 7 ADE86207
44 47 41.6 458 7 ADG87365
45 47 41.6 458 7 ADG88787

ALIGNMENTS

RESULT 1
AAB81158
ID AAB81158 standard; peptide; 25 AA.

AC AAB81158;

DT 13-JUL-2001 (first entry)

DE SlpA peptide from Corynebacterium ammoniagenes.

KW Coryneform bacteria; transglutaminase; food processing; SlpA.

OS Corynebacterium ammoniagenes.

PN WO200123591-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006780.

PR 30-SEP-1999; 99JP-00280098.

PR 28-JUN-2000; 2000JP-00194043.

XX (AJIN) AJINOMOTO CO INC.

XX Kikuchi Y, Date M, Umezawa Y, Yokoyama K, Matsui H;

XX WPI; 2001-266172/27.

PT Efficient secretory production of foreign proteins e.g. transglutaminase
PT employing transformant coryneform bacterium, simply on industrial scale
PT with direct recovery for use in food processing and pharmaceutical industry.

Claim 7; Page 77; 151pp Japanese.

This invention relates to a process for the production of a foreign secretory protein through the construction of a recombinant coryneform bacterium. The coryneform bacterium is transformed with an expression construct in which DNA encoding a target foreign protein pro-structure is ligated to the downstream region of DNA encoding the signal peptide domain of a coryneform bacterial protein. Following transformation with the vector, the bacterium is cultured, and the pro-peptide cleaved from the expressed protein. Transglutaminases produced using this process are useful in the food processing and pharmaceutical industries. The present sequence represents a corynebacterium ammoniagenes SlpA peptide, which is used in the method of the invention

```

SQ Sequence 25 AA;
Query Match 100.0%; Score 113; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAAPVATA 25
   |||||
DB 1 MKRMKSLAAALTAVAGAMLAAPVATA 25

RESULT 2
ABU07388
ID ABU07388 standard; peptide; 25 AA.
AC ABU07388;
XX
DT 28-JAN-2003 (first entry)
XX
DE Coryneform bacterium peptide #2.
XX
KW Coryneform bacterium; signal peptide domain; food processing; medicine;
KW cosmetic; transglutaminase; human epithelial growth factor.
XX
OS Corynebacterium ammoniagenes.
XX
FN WO200281694-A1.
XX
PD 17-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-JP002978.
XX
PR 30-MAR-2001; 2001JP-00098908.
XX
PA (AJIN ) AJINOMOTO CO INC.
XX
PI Kikuchi Y, Date M, Umezawa Y, Yokoyama K, Heima H, Matsui H;
XX
DR WPI; 2003-058550/05.
XX
PT Secretion production of foreign proteins by culturing transformant
PT coryneform bacteria, applicable in producing e.g. industrially-useful
PT transglutaminase and human epithelial growth factor.
XX
PS Claim 8; Page 60; 117pp; Japanese.
XX
CC The invention relates to a method for producing a foreign protein by
CC culturing a mutant strain of a coryneform bacterium that contains an
CC expression gene construct to secrete the foreign protein, followed by
CC recovery of the produced foreign protein. The gene construct is obtained
CC by ligation of a nucleic acid encoding a signal peptide domain
CC originating from a coryneform bacterium, to downstream of a functioning
CC promoter sequence in the coryneform bacterium and also by ligation of a
CC nucleic acid encoding a foreign protein, to downstream of a nucleic acid
CC sequence encoding the signal peptide. The method is useful for the
CC production of a foreign protein which is applicable in producing e.g.
CC industrially-useful transglutaminase and human epithelial growth factor
CC for use in medicine, cosmetics and food processing. This sequence
CC represents a coryneform bacterium protein of the invention
XX
SQ Sequence 25 AA;
Query Match 100.0%; Score 113; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAAPVATA 25
   |||||
DB 1 MKRMKSLAAALTAVAGAMLAAPVATA 25

RESULT 3
ADC64923
ID ADC64923 standard; peptide; 25 AA.
AC ADC64923;
XX
DT 18-DEC-2003 (first entry)
XX
DE Corynebacterium ammoniagenes signal peptide SEQ ID NO:3.
XX
KW Corynebacterium; human epidermal growth factor; hEGF; human;
KW epidermal growth factor; signal peptide; Corynebacterium ammoniagenes.
XX
OS Corynebacterium ammoniagenes.
XX
PN JP2002291476-A.
XX
PD 08-OCT-2002.
XX
PF 30-MAR-2001; 2001JP-00098802.
XX
PR 30-MAR-2001; 2001JP-00098802.
XX
PA (AJIN ) AJINOMOTO KK.
XX
DR WPI; 2003-317840/31.
XX
PT Preparation of human epidermal growth factor and a transformed
PT Corynebacterium used to produce the epidermal growth factor.
XX
PS Claim 7; Page 8; 11pp; Japanese.
XX
CC The present invention describes a transformed Corynebacterium having an
CC expression gene structure comprising a promoter sequence followed by a
CC nucleic acid sequence encoding a region containing a signal peptide
CC derived from Corynebacterium, followed by a nucleic acid sequence
CC encoding human epidermal growth factor (hEGF). Also described is a method
CC for the preparation of hEGF in which the above transformed
CC Corynebacterium is cultured to produce and secrete human EGF and then
CC secreted hEGF is recovered. The present sequence represents a
CC specifically claimed signal peptide derived from Corynebacterium
CC ammoniagenes, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 25 AA;
Query Match 100.0%; Score 113; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAAPVATA 25
   |||||
DB 1 MKRMKSLAAALTAVAGAMLAAPVATA 25

RESULT 4
AAW56155
ID AAW56155 standard; protein; 358 AA.
XX
AC AAW56155;
XX
DT 15-JUL-1998 (first entry)
XX
DE Aa cell surface layer protein of C. ammoniagenes.
XX
KW Cell surface layer protein; protein expression; extracellular secretion;
KW ss.
XX
OS Corynebacterium ammoniagenes.
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT Protein /note= "signal peptide"
FT /note= "mature protein"

```

XX JP10108675-A.
 XX 28-APR-1998.
 XX 07-OCT-1996; 96JP-00265661.
 XX 07-OCT-1996; 96JP-00285661.
 XX (AJIN) AJINOMOTO KK.
 XX WPI; 1998-304970/27.
 XX N-PSDB; AAU22667.
 XX New DNA isolated from Corynebacterium ammoniagenes encodes cell surface
 PT layer protein - and recombinant DNA, vector and host used to produce
 PT protein.
 XX
 XX Claim 1; Page 5-7; 8pp; Japanese.
 XX
 CC The present sequence represents a cell surface layer protein, and is
 CC isolated from Corynebacterium ammoniagenes AFCC6872. A gene of interest
 CC can be inserted downstream of the present sequence. Subsequent expression
 CC of the gene by the microbe causes it to be secreted extracellularly
 XX
 XX Sequence 358 AA;
 SQ
 Query Match 100.0%; Score 113; DB 2; Length 358;
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKMKSLAAALTVAGAMLAAPVATA 25
 |||||
 Db 1 MKMKSLAAALTVAGAMLAAPVATA 25
 |||||
 RESULT 5
 AAG92890
 ID AAG92890 standard; protein; 395 AA.
 XX
 AC AAG92890;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE C glutamicum protein fragment SEQ ID NO: 6644.
 XX
 KW Corynebacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN EP1108790-A2.
 XX
 PD 20-JUN-2001.
 XX
 PF 18-DEC-2000; 2000EP-00127688.
 XX
 PR 16-DEC-1999; 99JP-00377484.
 PR 07-APR-2000; 2000JP-00159162.
 PR 03-AUG-2000; 2000JP-00280988.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX
 XX WPI; 2001-376931/40.
 XX N-PSDB; AAH68109.
 XX Novel polynucleotides derived from Corynebacterium, for identifying
 PT mutation point of a gene, measuring expression of a gene, analyzing
 PT expression profile or pattern of a gene and identifying homologous gene.
 XX

PS Claim 17; SEQ ID NO 6644; 246pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and analysing
 CC the expression profile or expression pattern of a gene derived from
 CC Coryneform bacterium, and identifying a homologue of a gene derived from
 CC Coryneform bacterium. Coryneform bacteria are useful for producing amino
 CC acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a protein described in the
 CC exemplification of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from the European Patent Office
 XX
 XX Sequence 395 AA;
 SQ
 Query Match 50.4%; Score 57; DB 4; Length 395;
 Best Local Similarity 66.7%; Pred. No. 5.7;
 Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 KRMKSLAAALTVAGAMLA 19
 |||||
 Db 13 KRLKPLAAAVAVAGVLLA 30
 |||||
 RESULT 6
 AAG91111
 ID AAG91111 standard; protein; 104 AA.
 XX
 AC AAG91111;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE C glutamicum protein fragment SEQ ID NO: 4865.
 XX
 KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN EP1108790-A2.
 XX
 PD 20-JUN-2001.
 XX
 PF 18-DEC-2000; 2000EP-00127688.
 XX
 PR 16-DEC-1999; 99JP-00377484.
 PR 07-APR-2000; 2000JP-00159162.
 PR 03-AUG-2000; 2000JP-00280988.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX
 XX WPI; 2001-376931/40.
 XX N-PSDB; AAH66330.
 XX Novel polynucleotides derived from Coryneform bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analyzing
 PT expression profile or pattern of a gene and identifying homologous gene.
 XX
 XX Claim 17; SEQ ID NO 4865; 246pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and analysing
 CC the expression profile or expression pattern of a gene derived from
 CC Coryneform bacterium, and identifying a homologue of a gene derived from
 CC Coryneform bacterium. Coryneform bacteria are useful for producing amino
 CC acids, nucleic acids, vitamins, saccharides and organic acids,

CC particularly L-lysine. The present sequence is a protein described in the
 CC exemplification of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from the European Patent Office

XX SQ Sequence 104 AA;

Query March 45.1%; Score 51; DB 4; Length 104;
 Best Local Similarity 48.0%; Pred. No. 9.7;
 Matches 12; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MKRMKSLAALTVAGAMLAAPVATA 25
 Db 2 IKKYLSTIAAVTIAASAVLFAPSAQA 26

RESULT 7
 AAW32371
 ID AAW32371 standard; protein; 107 AA.

XX AC AAW32371;

XX DT 13-JAN-1998 (first entry)

XX DE Mycobacterium tuberculosis antigen TbrAB.

XX KW Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
 XX KW skin testing; M.tuberculosis.

XX OS Mycobacterium tuberculosis.

XX FH Key Location/Qualifiers

FT Misc-difference 60 /note= "Any amino acid"
 FT Misc-difference 64 /note= "Any amino acid"
 FT Misc-difference 73 /note= "Any amino acid"
 FT Misc-difference 77 /note= "Any amino acid"
 FT Misc-difference 79 /note= "Any amino acid"
 FT Misc-difference 86 /note= "Any amino acid"
 FT Misc-difference 99 /note= "Any amino acid"
 FT Misc-difference 102 /note= "Any amino acid"
 FT Misc-difference 103 /note= "Any amino acid"
 FT Misc-difference 106 /note= "Any amino acid"

XX PN WO9709429-A2.

XX PD 13-MAR-1997.

XX PF 30-AUG-1996; 96WO-US014675.

XX PR 01-SEP-1995; 95US-00523435.

XX PR 22-SEP-1995; 95US-00532136.

XX PR 22-MAR-1996; 96US-00620280.

XX PR 05-JUN-1996; 96US-00658800.

XX PR 12-JUL-1996; 96US-00680573.

XX PA (CORI-) CORIXA CORP.

XX PI Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;

XX PI Vedvick TH, Twardzik DR;

XX PR WPI; 1997-192904/17.

XX PR N-FSDB; AAT91418.

PT New immunogenic polypeptide(s) from soluble M. tuberculosis antigens -
 FT useful for diagnosis of M. tuberculosis infection.

XX Example 3; Page 131-132; 190pp; English.

XX CC A new immunogenic polypeptide has been developed comprising an
 CC immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its
 CC variant differing only in conservative substitutions and/or
 CC modifications). The present sequence represents a M.tuberculosis antigen,
 CC TbrAB. The immunogenic polypeptide can be used to diagnose M.tuberculosis
 CC infection by forming complexes with specific antibodies in the sample.
 CC Fragments of DNA encoding the immunogenic polypeptide can be used as
 CC diagnostic primers or probes and agents that bind to the antigen,
 CC especially monoclonal antibodies or equivalent polyclonal antibodies, are
 CC also used for diagnosis

XX SQ Sequence 107 AA;

Query March 45.1%; Score 51; DB 2; Length 107;
 Best Local Similarity 60.0%; Pred. No. 10;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAALTVAGAMLA 20

Db 10 MKVMKSLAAGLTAAAGAA 29

RESULT 8

AAW32439

ID AAW32439 standard; protein; 107 AA.

XX AC AAW32439;

XX DT 08-JAN-1998 (first entry)

XX DE Mycobacterium tuberculosis antigen TbrAB.

XX KW Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
 XX KW skin testing; M.tuberculosis.

XX OS Mycobacterium tuberculosis.

XX FH Key Location/Qualifiers

FT Misc-difference 60 /note= "Any amino acid"
 FT Misc-difference 64 /note= "Any amino acid"
 FT Misc-difference 73 /note= "Any amino acid"
 FT Misc-difference 77 /note= "Any amino acid"
 FT Misc-difference 79 /note= "Any amino acid"
 FT Misc-difference 86 /note= "Any amino acid"
 FT Misc-difference 99 /note= "Any amino acid"
 FT Misc-difference 102 /note= "Any amino acid"
 FT Misc-difference 103 /note= "Any amino acid"
 FT Misc-difference 106 /note= "Any amino acid"

XX PN WO9709428-A2.

XX PD 13-MAR-1997.

XX PF 30-AUG-1996; 96WO-US014674.

XX PR 01-SEP-1995; 95US-00523436.

XX PR 22-SEP-1995; 95US-00533634.

XX PR 22-MAR-1996; 96US-00620874.


```

PR 05-JUN-1996; 96US-00659683.
PR 12-JUL-1996; 96US-00680574.
XX
PA (CORI-) CORIXA CORP.
PI Read SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
PI Vedvick TH, Twardzik DR;
XX
XX WPI; 1997-192903/17.
DR N-PSDB; AAT91481.
XX
XX New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are
PT useful in vaccines for prevention or treatment of tuberculosis, also for
PT diagnosis.
PT
XX
XX Example 3; Page 120; 168pp; English.
XX
XX A new immunogenic polypeptide has been developed comprising an
CC immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its
CC variant differing only in conservative substitutions and/or
CC modifications). The present sequence represents a M.tuberculosis antigen,
CC TbrAB. The immunogenic protein, and fusion proteins containing one or
CC more of the proteins or one of the proteins plus ESAT-6, are useful in
CC vaccines, preferably when formulated with a non-specific adjuvant, to
CC induce an immune response against M.tuberculosis (for treatment or
CC prevention).
XX
XX Sequence 107 AA;
SQ
Query Match 45.1%; Score 51; DB 2; Length 107;
Best Local Similarity 60.0%; Pred. NO. 10;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAALTVAGAMLAA 20
DB 10 MKRMKSLAALTVAGAMLAA 29

RESULT 9
AAW64311
ID AAW64311 standard; protein; 107 AA.
XX
AC AAW64311,
XX
DT 17-OCT-2003 (revised)
DT 09-NOV-1998 (first entry)
XX
XX Mycobacterium tuberculosis antigen TbrAB.
XX
XX Tuberculosis; infection; diagnosis; antigen; TbrAB.
XX
XX Mycobacterium tuberculosis; strain H37Ra.
XX
XX Key Location/Qualifiers
FH Misc-difference 40
FT /note= "encoded by GGN"
FT Misc-difference 60
FT /note= "encoded by GAN"
FT Misc-difference 64
FT /note= "encoded by GAN"
FT Misc-difference 73
FT /note= "encoded by AGN"
FT Misc-difference 77
FT /note= "encoded by AGN"
FT Misc-difference 79
FT /note= "encoded by GNC"
FT Misc-difference 86
FT /note= "encoded by GNG"
FT Misc-difference 89
FT /note= "encoded by GGN"
FT Misc-difference 94
FT /note= "encoded by GGN"
FT Misc-difference 95

PR 05-JUN-1996; 96US-00659683.
PR 12-JUL-1996; 96US-00680574.
XX
PA (CORI-) CORIXA CORP.
PI Read SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
PI Vedvick TH, Twardzik DR;
XX
XX WPI; 1997-192903/17.
DR N-PSDB; AAT91481.
XX
XX New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are
PT useful in vaccines for prevention or treatment of tuberculosis, also for
PT diagnosis.
PT
XX
XX Example 3; Page 120; 168pp; English.
XX
XX A new immunogenic polypeptide has been developed comprising an
CC immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its
CC variant differing only in conservative substitutions and/or
CC modifications). The present sequence represents a M.tuberculosis antigen,
CC TbrAB. The immunogenic protein, and fusion proteins containing one or
CC more of the proteins or one of the proteins plus ESAT-6, are useful in
CC vaccines, preferably when formulated with a non-specific adjuvant, to
CC induce an immune response against M.tuberculosis (for treatment or
CC prevention).
XX
XX Sequence 107 AA;
SQ
Query Match 45.1%; Score 51; DB 2; Length 107;
Best Local Similarity 60.0%; Pred. NO. 10;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAALTVAGAMLAA 20
DB 10 MKRMKSLAALTVAGAMLAA 29

RESULT 10
AAW81674
ID AAW81674 standard; protein; 107 AA.
XX
AC AAW81674;
XX
DT 27-JAN-1999 (first entry)
XX
Query Match 45.1%; Score 51; DB 2; Length 107;
Best Local Similarity 60.0%; Pred. NO. 10;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAALTVAGAMLAA 20
DB 10 MKRMKSLAALTVAGAMLAA 29

RESULT 10
AAW81674
ID AAW81674 standard; protein; 107 AA.
XX
AC AAW81674;
XX
DT 27-JAN-1999 (first entry)
XX

```

DE M. tuberculosis immunogenic polypeptide TbrA3.
 XX
 KW Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB;
 KW vaccine; pharmaceutical; infection; diagnosis.
 XX
 OS Mycobacterium tuberculosis.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 60 /label= unknown
 FT Misc-difference 64 /label= unknown
 FT Misc-difference 73 /label= unknown
 FT Misc-difference 77 /label= unknown
 FT Misc-difference 79 /label= unknown
 FT Misc-difference 86 /label= unknown
 FT Misc-difference 99 /label= unknown
 FT Misc-difference 102 /label= unknown
 FT Misc-difference 103 /label= unknown
 FT Misc-difference 106 /label= unknown
 FT Misc-difference 107 /label= unknown
 XX WO9816646-A2.
 XX
 XX 23-APR-1998.
 XX
 XX 07-OCT-1997; 97WO-US018293.
 XX
 XX 11-OCT-1996; 96US-00730510.
 XX 13-MAR-1997; 97US-00818112.
 XX (CORI-) CORIXA CORP.
 XX
 XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
 PI Vedvick TS, Twardzik DR, Lodes MJ;
 XX WPI; 1998-261042/23.
 XX N-PSDB; AAV64467.
 XX
 XX Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to
 PT develop products for the detection of M. tuberculosis infection and for
 PT diagnosis, treatment and prevention of tuberculosis.
 XX
 XX Example 3; Page 115; 230pp; English.
 XX
 CC This sequence represents an immunogenic portion of a soluble
 CC Mycobacterium tuberculosis (MT) antigen which can be used in a method for
 CC inducing protective immunity against tuberculosis (TB). This sequence can
 CC be formulated into vaccines and/or pharmaceutical compositions for
 CC immunising against M. tuberculosis infection or may be used for the
 CC diagnosis of tuberculosis
 XX
 XX Sequence 107 AA;
 XX
 Query Match 45.1%; Score 51; DB 2; Length 107;
 Best Local Similarity 60.0%; Pred. No. 10;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MKRMKSLAALTVAGAMLAA 20
 DB 10 MKMKVSTAAAGLTAAGAA 29
 RESULT 11
 AAV38976
 ID AAV38976 standard; protein; 107 AA.

XX AAV38976;
 AC
 XX 05-NOV-1999 (first entry)
 DT
 XX M. tuberculosis recombinant antigen protein TbrA3.
 DE
 XX Antigen; diagnosis; detection; infection; antibody; immunisation;
 KW vaccine; immunity.
 KW
 XX Mycobacterium tuberculosis.
 OS
 XX WO9942118-A2.
 PN
 XX 26-AUG-1999.
 PD
 XX 17-FEB-1999; 99WO-US003265.
 PF
 XX 18-FEB-1998; 98US-00024753.
 PR
 XX 05-MAY-1998; 98US-00072596.
 XX
 XX (CORI-) CORIXA CORP.
 PA
 XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
 PI Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
 XX WPI; 1999-527416/44.
 DR
 XX N-PSDB; AAZ19057.
 XX
 XX New polypeptide comprising antigenic portions of M. tuberculosis.
 PT
 XX Example 3; Page 156; 323pp; English.
 PS
 XX This invention describes novel recombinant antigens and their encoding
 CC nucleic acids derived from Mycobacterium tuberculosis. The novel
 CC polypeptides are useful for detecting M. tuberculosis infection in a
 CC biological sample by detecting antibodies which bind with the
 CC polypeptides, and are useful as vaccines for immunizing against M.
 CC tuberculosis infection. The new detection methods are needed as current
 CC vaccination strategies do not provide 100% immunity
 XX
 XX Sequence 107 AA;
 XX
 Query Match 45.1%; Score 51; DB 2; Length 107;
 Best Local Similarity 60.0%; Pred. No. 10;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MKRMKSLAALTVAGAMLAA 20
 DB 10 MKMKVSTAAAGLTAAGAA 29
 RESULT 12
 AAV39113
 ID AAV39113 standard; protein; 107 AA.
 XX
 XX AAV39113;
 AC
 XX 05-NOV-1999 (first entry)
 DT
 XX M. tuberculosis antigen TbrA3 amino acid sequence.
 DE
 XX Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
 KW immunotherapy; diagnosis; immunisation; vaccine; infection;
 KW immune response; skin test.
 XX
 XX Mycobacterium tuberculosis.
 OS
 XX WO9942076-A2.
 PN
 XX 26-AUG-1999.
 PD
 XX 17-FEB-1999; 99WO-US003268.
 PF

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XX 18-FEB-1998; 98US-00025197.
PR 05-MAY-1998; 98US-00072967.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
PI Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
XX
XX WPI; 1999-527409/44.
DR N-PSDB; AA219269.
XX
XX New antigens from Mycobacterium tuberculosis useful in diagnostic skin
PT tests and protective or therapeutic vaccines or compositions.
PT
XX Example 3; Page 111; 299pp; English.
XX
XX The present invention describes polypeptides comprising an immunogenic
CC part of a Mycobacterium tuberculosis antigen (Ag). Also described are
CC vaccines and fusion protein containing M. tuberculosis Ag's. M.
CC tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other
CC polypeptides fragments, can be used in pharmaceutical compositions or
CC vaccines to generate a protective or therapeutic immune response to M.
CC tuberculosis and as reagents in skin tests for diagnosis of tuberculosis.
CC Ag can induce proliferation of, or cytokine secretion by, T, B or natural
CC killer cells and/or macrophages in tuberculosis-immune subjects. AA219249
CC to AA219460 and AA239083 to AA239225 are used in the exemplification of
CC the present invention
XX
XX Sequence 107 AA;
SQ
Query Match 45.1%; Score 51; DB 2; Length 107;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
   |||:|||||:|:|
Db 10 MKMKVKSIAAGLTAAAGAA 29

RESULT 13
AAW32393
ID AAW32393 standard; protein; 168 AA.
XX
XX AAW32393;
XX
XX 12-JAN-1998 (first entry)
XX
XX Mycobacterium tuberculosis antigen DPAS.
XX
XX Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
KW skin testing; M.tuberculosis.
XX
XX Mycobacterium tuberculosis.
OS
XX WO9709429-A2.
XX
XX 13-MAR-1997.
XX
XX 30-AUG-1996; 96WO-US014675.
XX
XX 01-SEP-1995; 95US-00523435.
XX
XX 22-SEP-1995; 95US-00532136.
XX
XX 22-MAR-1996; 96US-00620280.
XX
XX 05-JUN-1996; 96US-00658800.
XX
XX 12-JUL-1996; 96US-00680573.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
PI Vedvick TH, Twardzik DR;
XX
XX WPI; 1997-192904/17.
DR

XX 18-FEB-1998; 98US-00025197.
PR 05-MAY-1998; 98US-00072967.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
PI Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
XX
XX WPI; 1999-527409/44.
DR N-PSDB; AA219269.
XX
XX New antigens from Mycobacterium tuberculosis useful in diagnostic skin
PT tests and protective or therapeutic vaccines or compositions.
PT
XX Example 3; Page 111; 299pp; English.
XX
XX The present invention describes polypeptides comprising an immunogenic
CC part of a Mycobacterium tuberculosis antigen (Ag). Also described are
CC vaccines and fusion protein containing M. tuberculosis Ag's. M.
CC tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other
CC polypeptides fragments, can be used in pharmaceutical compositions or
CC vaccines to generate a protective or therapeutic immune response to M.
CC tuberculosis and as reagents in skin tests for diagnosis of tuberculosis.
CC Ag can induce proliferation of, or cytokine secretion by, T, B or natural
CC killer cells and/or macrophages in tuberculosis-immune subjects. AA219249
CC to AA219460 and AA239083 to AA239225 are used in the exemplification of
CC the present invention
XX
XX Sequence 107 AA;
SQ
Query Match 45.1%; Score 51; DB 2; Length 168;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGAMLAA 20
   |||:|||||:|:|
Db 1 MKMKVKSIAAGLTAAAGAA 20

RESULT 14
AAW32465
ID AAW32465 standard; protein; 168 AA.
XX
XX AAW32465;
XX
XX 09-JAN-1998 (first entry)
XX
XX Mycobacterium tuberculosis antigen DPAS.
XX
XX Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
KW skin testing; M.tuberculosis.
XX
XX Mycobacterium tuberculosis.
OS
XX WO3709428-A2.
XX
XX 13-MAR-1997.
XX
XX 30-AUG-1996; 96WO-US014674.
XX
XX 01-SEP-1995; 95US-00523436.
XX
XX 22-SEP-1995; 95US-00533634.
XX
XX 22-MAR-1996; 96US-00620874.
XX
XX 05-JUN-1996; 96US-00659683.
XX
XX 12-JUL-1996; 96US-00680574.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Skeiky YA, Dillon DC, Campos-Neto A, Houghton R;
PI Vedvick TH, Twardzik DR;
XX
XX WPI; 1997-192903/17.
DR N-PSDB; AA291487.
XX
XX New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are
PT useful in vaccines for prevention or treatment of tuberculosis, also for
PT diagnosis.
XX
XX Disclosure; Page 132-133; 168pp; English.
XX

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AC AAY38986;
XX 05-NOV-1999 (first entry)
DT M. tuberculosis recombinant antigen protein DPAS.
XX Antigen; diagnosis; detection; infection; antibody; immunisation;
XX vaccine; immunity.
KW Mycobacterium tuberculosis.
XX WO9942118-A2.
XX 26-AUG-1999.
XX 17-FEB-1999; 99WO-US003265.
XX 18-FEB-1998; 98US-00024753.
XX 05-MAY-1998; 98US-00072596.
XX (CORI-) CORIXA CORP.
PA Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
PI Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
XX WPI; 1999-527416/44.
XX N-PSDB; AAZ19089.
XX New polypeptide comprising antigenic portions of M. tuberculosis.
XX Claim 3; Page 163-164; 323pp; English.
XX This invention describes novel recombinant antigens and their encoding
CC nucleic acids derived from Mycobacterium tuberculosis. The novel
CC polypeptides are useful for detecting M. tuberculosis infection in a
CC biological sample by detecting antibodies which bind with the
CC polypeptides, and are useful as vaccines for immunizing against M.
CC tuberculosis infection. The new detection methods are needed as current
CC vaccination strategies do not provide 100% immunity
XX
XX Sequence 168 AA;
Query Match 45.1%; Score 51; DB 2; Length 168;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 MKRMKSLAAALTIVAGAVLAA 20
||:|||||:|
Db 1 MKMKVKSIAAGLTAAGAA 20
RESULT 18
AAY39129
ID AAY39129 standard; protein; 168 AA.
XX AAY39129;
XX 05-NOV-1999 (first entry)
XX M. tuberculosis antigen DPAS amino acid sequence.
XX Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
XX immunotherapy; diagnosis; immunisation; vaccine; infection;
XX immune response; skin test.
XX Mycobacterium tuberculosis.
XX WO9942076-A2.
XX 26-AUG-1999.
XX 17-FEB-1999; 99WO-US003268.
XX

PR 18-FEB-1998; 98US-00025197.
PR 05-MAY-1998; 98US-00072967.
XX (CORI-) CORIXA CORP.
XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
PI Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
XX WPI; 1999-527409/44.
XX N-PSDB; AAZ19301.
XX New antigens from Mycobacterium tuberculosis useful in diagnostic skin
XX tests and protective or therapeutic vaccines or compositions.
XX Disclosure; Page 118-119; 293pp; English.
XX The present invention describes polypeptides comprising an immunogenic
XX part of a Mycobacterium tuberculosis antigen (Ag). Also described are
XX vaccines and fusion protein containing M. tuberculosis Ag's. M.
XX tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other
XX polypeptides fragments, can be used in pharmaceutical compositions or
XX vaccines to generate a protective or therapeutic immune response to M.
XX tuberculosis and as reagents in skin tests for diagnosis of tuberculosis.
XX Ag can induce proliferation of, or cytokine secretion by, T, B or natural
XX killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249
XX to AAZ19460 and AAY39083 to AAY39225 are used in the exemplification of
XX the present invention
XX
XX Sequence 168 AA;
Query Match 45.1%; Score 51; DB 2; Length 168;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 MKRMKSLAAALTIVAGAVLAA 20
||:|||||:|
Db 1 MKMKVKSIAAGLTAAGAA 20
RESULT 19
AAB52454
ID AAB52454 standard; protein; 168 AA.
XX AAB52454;
XX 23-FEB-2001 (first entry)
XX Mycobacterium tuberculosis secreted protein #19.
XX Mycobacterium tuberculosis secreted protein; MTSP; vaccine.
XX Mycobacterium tuberculosis.
XX WO200066143-A1.
XX 09-NOV-2000.
XX 04-MAY-2000; 2000WO-US012197.
XX 04-MAY-1999; 98US-0132479P.
XX 04-MAY-1999; 98US-0132503P.
XX (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
XX Gennaro ML, Gomez MJ;
XX WPI; 2001-007151/01.
XX Novel Mycobacterium tuberculosis secreted polypeptides and
XX polynucleotides useful in diagnosis, treatment and prophylaxis of
XX tuberculosis.
XX Claim 11; Fig 1; 60pp; English.
XX

XX
CC The present invention relates to Mycobacterium tuberculosis secreted
CC proteins (MTSP), where the polypeptide has M. tuberculosis specific
CC antigenic and immunogenic properties. Compositions of the invention may
CC be useful for diagnosing Mycobacterium tuberculosis infection and as a
CC vaccine against M. tuberculosis infection
XX
SQ Sequence 168 AA;

Query Match 45.1%; Score 51; DB 4; Length 168;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAALTAVAGMLAA 20
Db 1 MKMKVKSIAAGLTAAAAIGAA 20
||:|||||:|

RESULT 20
ABU05883
ID ABU05883 standard; protein; 168 AA.
XX
AC ABU05883;
XX
XX 08-APR-2003 (first entry)
XX
DE M. tuberculosis and M. leprae marker protein #534.
XX
XX Mycobacterioses; survival; virulence; protective antigen; vaccine;
KW Mycobacterial disease; tuberculosis; leprosy.
XX
OS Mycobacterium tuberculosis.
OS Mycobacterium leprae.
XX
XX WO200274903-A2.
XX
XX 26-SEP-2002.
XX
XX 22-FEB-2002; 2002WO-IB001973.
XX
XX 22-FEB-2001; 2001US-0270123P.
XX
XX (INSP) INST PASTEUR.
XX
XX Cole S;
XX
XX WPI; 2002-759885/82.
XX
XX Identifying and selecting genes for survival or virulence of mycobacteria
XX by a comparative genomic analysis of the sequences of Mycobacterium
XX tuberculosis and M. leprae.
XX
XX Claim 17; Page 744; 874pp; English.
XX
XX This invention relates to a novel method for identifying essential genes
XX for survival or virulence of mycobacteria species. The method comprises
XX aligning the genomic sequence of a first mycobacterium species on a
XX genomic sequence of a second mycobacterium species and selecting a
XX polynucleotide sequence that is highly conserved in both genomes with no
XX counterparts in other bacterial genomic sequences and that corresponds to
XX an essential gene for the survival or virulence of mycobacterium species.
XX The method of the invention is useful for detecting M. tuberculosis or M.
XX leprae infection. The method reduces the number of potential new targets
XX and protective antigens for new drugs and vaccine compositions to treat
XX and prevent mycobacterial diseases, particularly tuberculosis and
XX leprosy. The present sequence represents a marker protein from
XX Mycobacterium tuberculosis and Mycobacterium leprae identified using the
XX method of the invention
XX
SQ Sequence 168 AA;

Query Match 45.1%; Score 51; DB 5; Length 168;
Best Local Similarity 60.0%; Pred. No. 17;

Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAALTAVAGMLAA 20
Db 1 MKMKVKSIAAGLTAAAAIGAA 20
||:|||||:|

RESULT 21
AAW32351
ID AAW32351 standard; protein; 186 AA.
XX
AC AAW32351;
XX
XX 13-JAN-1998 (first entry)
XX
DE Mycobacterium tuberculosis antigen TbRa1.
XX
KW Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
KW skin testing; M. tuberculosis.
XX
OS Mycobacterium tuberculosis.
XX
XX WO9709429-A2.
XX
XX 13-MAR-1997.
XX
XX 30-AUG-1996; 96WO-US014675.
XX
XX 01-SEP-1995; 95US-00523435.
PR 22-SEP-1995; 95US-00523136.
PR 22-MAR-1996; 96US-00620280.
PR 05-JUN-1996; 96US-00658800.
PR 12-JUL-1996; 96US-00680573.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
XX Vedwick TH, Twardzik DR;
XX WPI; 1997-192904/17.
XX N-PSDB; AAT91401.
XX
XX New immunogenic polypeptide(s) from soluble M. tuberculosis antigens -
XX useful for diagnosis of M. tuberculosis infection.
XX
XX Example 3; Page 99-100; 190pp; English.
XX
XX A new immunogenic polypeptide has been developed comprising an
XX immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its
XX variant differing only in conservative substitutions and/or
XX modifications). The present sequence represents a M. tuberculosis antigen,
XX TbRa1. The immunogenic polypeptide can be used to diagnose M. tuberculosis
XX infection by forming complexes with specific antibodies in the sample.
XX Fragments of DNA encoding the immunogenic polypeptide can be used as
XX diagnostic primers or probes and agents that bind to the antigen,
XX especially monoclonal antibodies or equivalent polyclonal antibodies, are
XX also used for diagnosis
XX
XX Sequence 186 AA;

Query Match 45.1%; Score 51; DB 2; Length 186;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAALTAVAGMLAA 20
Db 20 MKMKVKSIAAGLTAAAAIGAA 39
||:|||||:|

RESULT 22
AAW32419
ID AAW32419 standard; protein; 186 AA.
XX

```

AC AAW32419;
XX
XX 08-JAN-1998 (first entry)
XX
XX Mycobacterium tuberculosis antigen TbrAl.
XX
XX Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
XX skin testing; M.tuberculosis.
XX
XX Mycobacterium tuberculosis.
XX
XX OS
XX
XX WO9709428-A2.
XX
XX 13-MAR-1997.
XX
XX 30-AUG-1996; 96WO-US014674.
XX
XX 01-SEP-1995; 95US-00523436.
XX
XX 22-SEP-1995; 95US-00533634.
XX
XX 22-MAR-1996; 96US-00620874.
XX
XX 05-JUN-1996; 96US-00659683.
XX
XX 12-JUL-1996; 96US-00680574.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
XX Vedvick TH, Twardzik DR;
XX
XX WPI; 1997-192903/17.
XX
XX N-PSDB; AAT91464.
XX
XX New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are
XX useful in vaccines for prevention or treatment of tuberculosis, also for
XX diagnosis.
XX
XX Example 3; Page 93; 168pp; English.
XX
XX A new immunogenic polypeptide has been developed comprising an
XX immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its
XX variant differing only in conservative substitutions and/or
XX modifications). The present sequence represents a M.tuberculosis antigen,
XX TbrAl. The immunogenic protein, and fusion proteins containing one or
XX more of the proteins or one of the proteins plus ESAT-6, are useful in
XX vaccines, preferably when formulated with a non-specific adjuvant, to
XX induce an immune response against M.tuberculosis (for treatment or
XX prevention)
XX
XX SQ Sequence 186 AA;
XX
XX Query Match 45.1%; Score 51; DB 2; Length 186;
XX Best Local Similarity 60.0%; Pred. No. 19;
XX Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 MKRMKSLAALTVAGAMLAA 20
XX ||:|||||:|||||:|||||
XX Db 20 MKVMKSIAGLTAAGAAIGAA 39
XX
XX RESULT 24
XX AAW64291
XX ID AAW64291 standard; protein; 187 AA.
XX
XX AC AAW64291;
XX
XX 17-OCT-2003 (revised)
XX DT 09-NOV-1998 (first entry)
XX
XX Mycobacterium tuberculosis antigen TbrAl.
XX
XX Tuberculosis; infection; diagnosis; antigen; TbrAl.
XX
XX Mycobacterium tuberculosis; strain H37Ra.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 187
XX FT /note= "encoded by NAA"
XX
XX WO9816645-A2.
XX
XX 23-APR-1998.
XX
XX 07-OCT-1997; 97WO-US018214.
XX
XX 11-OCT-1996; 96US-00729622.
XX
XX 13-MAR-1997; 97US-00818111.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
XX Vedvick TS, Twardzik DR, Lodes MJ;
XX

```


CC coryneform bacterium. Coryneform bacteria are useful for producing amino
 CC acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a protein described in the
 CC exemplification of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from the European Patent Office

QQ Sequence 279 AA;

Query Match 44.2%; Score 50; DB 4; Length 279;
 Best Local Similarity 48.0%; Pred No. 41;
 Matches 12; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MKRMKSLAALTVAGAMLAAPVATA 25
 Db 1 MNRFPFALLAASVAGAAIAPATSA 25

RESULT 29

ADM20157
 ID ADM20157 standard; protein; 248 AA.

XX AC ADM20157;

XX DT 20-MAY-2004 (first entry)

XX DE Protein encoded by novel human channel/transporter gene #268 clone 2.
 XX KW immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
 KW cytoskeletal; cardiac; vasotropic; cerebroprotective; nootropic;
 KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
 KW gene therapy; channel/transporter protein; rheumatoid arthritis;
 KW neoplasm; cardiac arrest; cerebrovascular disorder; cerebral ischemia;
 KW angiogenesis; nervous system disorder; Alzheimer's disease;
 KW ocular disorder; corneal infection; wound healing;
 KW epithelial cell proliferation; skin aging; sunburn; transplantation;
 KW chemotaxis; food additive.

XX OS Homo sapiens.

XX DN W200154472-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001307.

XX PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180828P.

PR 24-FEB-2000; 2000US-0184564P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226688P.
 PR 23-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 29-SEP-2000; 2000US-0236371P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239355P.
 PR 13-OCT-2000; 2000US-0239377P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.

Query Match 43.4%; Score 49; DB 4; Length 378;
Best Local Similarity 50.0%; Pred. No. 82;
Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGMLAAPVAT 24
||| | : ||||| : : ||
Db 40 MKRSKRIAAALTSUTTIIVATAFAT 63

RESULT 31
ABM50663
ID ABM50663 standard; protein; 378 AA.

XX AC ABM50663;

XX DT 20-OCT-2003 (first entry)

XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #15339.

XX KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX KW immunostimulant; immune response; vaccine.

XX OS Propionibacterium acnes.

XX PN WO2003033515-A1.

XX PD 24-APR-2003.

XX PF 11-OCT-2002; 2002WO-US032727.

XX PR 15-OCT-2001; 2001US-00978825.

XX PA (CORI-) CORIXA CORP.

XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallie-Douglas J;

XX DR WPI; 2003-381789/36.
XX DR N-PSDB; ACF64492.

XX PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
XX PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
XX PT or for stimulating an immune response specific for a P. acnes protein.

XX PS Example 1; SEQ ID NO 15339; 1481pp; English.

XX CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
XX CC encoding a Propionibacterium acnes protein. The invention also relates to
XX CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
XX CC immunogenic fragments of P. acnes polypeptides. The invention
XX CC additionally encompasses expression vectors and host cells comprising a
XX CC polynucleotide of the invention, antibodies against polypeptides of the
XX CC invention; fusion proteins comprising a polypeptide of the invention; a
XX CC method for stimulating an immune response specific for a P. acnes
XX CC polypeptide and an isolated T cell population comprising T cells prepared
XX CC via this method; a vaccine composition (comprising P. acnes polypeptides,
XX CC polynucleotides, antibodies, fusion proteins, T cell populations, or
XX CC antigen-presenting cells that express the polypeptide); a method and kit
XX CC for detecting or determining the presence or absence of P. acnes in a
XX CC patient; and a method for inhibiting the development of P. acnes in a
XX CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
XX CC proteins, T cell populations or antigen-presenting cells that express the
XX CC polypeptides are useful for diagnosing, preventing or treating acne
XX CC vulgaris, or for stimulating an immune response specific for a P. acnes
XX CC protein. The polynucleotides can also be used as probes or primers for
XX CC nucleic acid hybridisation. The vaccine composition is useful for the
XX CC stimulation of an immune response against P. acnes, or for treating acne,
XX CC and the kit is useful for performing a diagnostic assay. The present
XX CC sequence represents a polypeptide predicted to be encoded by an ORF (open
XX CC reading frame) contained within the P. acnes polynucleotides of the
XX CC invention. Note: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 378 AA;

Query Match 43.4%; Score 49; DB 6; Length 378;
Best Local Similarity 50.0%; Pred. No. 82;
Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTAVAGMLAAPVAT 24
||| | : ||||| : : ||
Db 40 MKRSKRIAAALTSUTTIIVATAFAT 63

RESULT 32

ABG29771

ID ABG29771 standard; protein; 895 AA.

XX AC ABG29771;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #29762.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS93958.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.

XX PS Claim 20; SEQ ID NO 60130; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX CC and in recombinant production of (II). The polynucleotides are also used
XX CC in diagnostics as expressed sequence tags for identifying expressed
XX CC genes. (I) is useful in gene therapy techniques to restore normal
XX CC activity of (II) or to treat disease states involving (II). (II) is
XX CC useful for generating antibodies against it, detecting or quantitating a
XX CC polypeptide in tissue, as molecular weight markers and as a food
XX CC supplement. (II) and its binding partners are useful in medical imaging
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders
XX CC involving aberrant protein expression or biological activity. The
XX CC polypeptide and polynucleotide sequences have application in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
XX CC amino acid sequences of the invention. Note: The sequence data for this
XX CC patent did not appear in the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 895 AA;
 Query Match 43.4%; Score 49; DB 4; Length 895;
 Best Local Similarity 47.6%; Pred. No. 2.2e+02;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 RKMSLAALTVAGAMLAAPVA 23
 Db 671 RLTMAVAVTIAAILAFEMA 691

RESULT 33
 ADJ49642
 ID ADJ49642 standard; protein; 132 AA.
 XX AC ADJ49642;
 XX DT 06-MAY-2004 (first entry)
 XX DE Oil-associated gene related protein #1142.
 XX DE oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
 XX OS Unidentified.
 XX PN US2004025202-A1.
 XX PD 05-FEB-2004.
 XX PF 14-MAR-2003; 2003US-00389566.
 XX PR 15-MAR-2002; 2002US-0365301P.
 XX PR 26-JUN-2002; 2002US-0391786P.
 XX PR 26-JUN-2002; 2002US-0392018P.
 XX (LAUR/) LAURIE C C.
 XX PA (RAVA/) RAVANELLO M.
 XX PA (SAVA/) SAVAGE T.
 XX PA (LEDE/) LEDEUX J R.
 XX PA (ROGE/) ROGERS J A.
 XX PI Laurie CC, Ravanello M, Savage T, Ledoux JR, Rogers JA;
 XX WPI; 2004-142683/14.
 XX DR Novel recombinant DNA construct comprising a promoter functional in
 PT plants operably linked to an oil-associated gene for producing transgenic
 PT plant seed.
 XX Example 3; SEQ ID NO 1646; 22pp; English.

XX SQ Sequence 132 AA;
 Query Match 42.5%; Score 48; DB 8; Length 132;
 Best Local Similarity 57.9%; Pred. No. 35;
 Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 7 LAALTVAGAMLAAPVATA 25
 Db 33 VSAAPVGGMVAAPVAGA 51

RESULT 34
 ADJ34916
 ID ADJ34916 standard; protein; 405 AA.
 XX AC ADJ34916;
 XX DT 22-APR-2004 (first entry)
 XX DE Xylanase from an environmental sample seq id 132.
 XX DE antibacterial; fungicide; thermostable xylanase activity;
 KW dough conditioning; beverage production; nutritional supplement;
 KW animal feed; lignin reduction; wood product; xylan; bacterial infection;
 KW fungal infection; coccidiosis.
 XX OS Unidentified.
 XX PN WO2003106654-A2.
 XX PD 24-DEC-2003.
 XX PF 16-JUN-2003; 2003WO-US019153.
 XX PR 14-JUN-2002; 2002US-0389299P.
 XX PA (DIVE-) DIVERSA CORP.
 XX PI Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
 PI Esteghalalian A;
 XX WPI; 2004-099016/10.
 XX N-PSDB; ADJ34915.
 XX DR Novel xylanase recombinant polypeptide useful for improving textile
 PT texture, treating paper, eliminating microorganisms.
 XX Claim 60; SEQ ID NO 132; 570pp; English.
 XX The invention describes an isolated or recombinant polypeptide (I),
 CC having 50% or more identity to 190 300-1200 residue amino acid sequences
 CC (S1), given in the specification, over a region of 100 or more residues
 CC and the polypeptide as thermostable xylanase activity. (I) is useful for:
 CC dough conditioning; beverage production; as a nutritional supplement in
 CC animal feed; reducing lignin in a wood or a wood product; and for
 CC eliminating and protecting animals from a microorganism comprising xylan.
 CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
 CC acid encoding a polypeptide having a xylanase activity which involves
 CC amplification of a template nucleic acid with a primer pair capable of
 CC amplifying (II) or its subsequence. (I) is useful for treating and
 CC preventing bacterial infection and fungal infection e.g. coccidiosis.
 CC This is the amino acid sequence of a xylanase protein isolated from an
 CC environmental sample.
 XX SQ Sequence 405 AA;
 Query Match 42.5%; Score 48; DB 8; Length 405;
 Best Local Similarity 47.8%; Pred. No. 1.2e+02;
 Matches 11; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 KRMSLAALTVAGAMLAAPVAT 24
 Db 19 RQLTLAAAVTLAGATAAEEAT 41

RESULT 35
 ABU22871
 ID ABU22871 standard; protein; 998 AA.
 XX AC ABU22871;
 XX DT 19-JUN-2003 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #8398.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW Bordetella pertussis.
XX WO200277183-A2.
XX 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
DR N-PSDB; ACA26741.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 50795; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC from ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 998 AA;
Query Match 42.5%; Score 48; DB 6; Length 998;
Best Local Similarity 52.4%; Pred. No. 3.4e+02;
Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 3 RMKSLAAALTGAGMLAAPVA 23
DB 9 RHALAALALAGMARLAPAA 29

RESULT 36
ABU38409
ID ABU38409 standard; protein; 1234 AA.
XX AC ABU38409;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #23936.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Pseudomonas aeruginosa.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
DR N-PSDB; ACA2279.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 66333; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC from ftp.wipo.int/pub/published_pct_sequences
XX

Query Match 42.5%; Score 48; DB 7; Length 1234;

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*
CC *K. pneumoniae*, *P. aeruginosa*. The present sequence is encoded by one of
CC the target brokayou essential Nucleotide sequence data bank (NCBI) patents
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC http://wipo.int/pub/published_pct_sequences
CC
CC
CC Sequence 260 AA:

Sequence 260 AA:

Query Match	41.6%	Score 47;	DB 6;	Length 260;
Best Local Similarity	50.0%	Pred. No. 1.1e+02;		
Matches 11; Conservative	4;	Mismatches 7;	Indels 0;	Gaps 0;

QY 1 MKRMKSLAAALTVAGAMLAPV 22

1 MRFLGSLLLALSITGAHAAPV 22

RESULT 39
ABU21338
ID ABU21338 standard: protein: 409 AA.

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #6865.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

AA Burkholderia fungorum.

AA WO200277183-A2.
PN

XX
PD
03-OCT-2002.

21-MAR-2002: 2002WO-US009107.

XX
PR 21-MAR-2001: 2001US-00815242-

PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P

XX
PA (EJ.TT-) EJ.TTRA PHARM TNCXX
PT Wang T. Zamudio C. Malone C.

PI Wall D, Trawick JD, Car
yy

DR WPI; 2003-029926/02.
DR NI-PENB. AC25208

XX
DT
Nov: anti-cancer drugs]

PT for homologous nucle-

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[illegible]

the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell, also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies

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FT	Modified-site	146..150
FT		/label= N-glycosylation site
FT	Modified-site	151..157
FT		/label= N-myristoylation site
FT	Modified-site	161..167
FT		/label= N-myristoylation site
FT	Modified-site	168..172
FT		/label= N-glycosylation site
FT	Modified-site	267..271
FT		/label= N-glycosylation site
FT	Domain	286..308
FT		/label= Leucine zipper pattern
FT	Modified-site	446..452
FT		/label= N-myristoylation site
XX		
PN	WC200140465-A2.	
XX		
XX		
PD	07-JUN-2001.	
XX		
XX	10-NOV-2000; 2000WC-US030873.	
XX		
PR	30-NOV-1999; 99WC-US028313.	
PR	09-DEC-1999; 99US-0170262P.	
PR	23-DEC-1999; 99US-0172059P.	
PR	11-JAN-2000; 2000US-0175481P.	
PR	20-JAN-2000; 2000US-0177118P.	
PR	18-FEB-2000; 2000WC-US004342.	
PR	03-MAR-2000; 2000US-0187202P.	
PR	30-MAY-2000; 2000WC-US014941.	
PR	05-JUN-2000; 2000US-0209832P.	
PR	24-AUG-2000; 2000WC-US023328.	
XX		
XX	(GETH) GENENTECH INC.	
XX		
PI	Pong S, Goddard A, Godowski PJ, Grimaldi CJ,	
PI	Hillman KJ, Tumas D, Watanabe CK, Wood WI,	
XX		
DR	WPI; 2001-381384/40.	
DR	N-PSDB; AAC85957.	

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Query Match          41.6%; Score 47; DB 4; Length 458;
Best Local Similarity 59.1%; Pred. No. 2e+02;
Matches 13; Conservative 1; Mismatches 8; Indels

Qy 4 MKSLAAALTVGAMLAAPVATA 25
    |:|:|:|:|:|:|:|:|:|
Db 1 MRGLAVLLTVALLTLLAPGAGA 22

Search completed: December 1, 2004, 11:46:57
Job time : 156 secs

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